



```
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 45584
; LENGTH: 896
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-282-122A-45584

Query Match
Best Local Similarity 7.0%; Score 243; DB 12; Length 896;
Matches 132; Conservative 93; Mismatches 250; Indels 120; Gaps 29;

QY 113 XGYFDYKIDINQWPKVDNEVRWQ-----LHRVKKWQAMALVHATGDEKYAREWVYQY 167
Db 47 FGSSSYNLINW-----NEQERGVRLIHGHTFLGCLIAAYNDTGDMYIKKSIBLI 99
QY 168 SDWARKNPLGLSQDNDFWVRPLEVSDRVQSLPPTFSFLVNSPAPTPAFME-----FLN 222
Db 100 KWINNHSFELHQHSMAR-----HDETTAL--RLQWLRFYFTROVLSEEBILILEK 150
QY 223 SYHQOADYLSHY--AEOGNHLEFAQNLFAGVSFPFEK--DSP---RWRQTGISVLNTE 276
Db 151 SMEDTAKLLSDDFFHATNTNMGFQ--DRALLTYASY--FKGENPSLEKYIKLAVTRUKDY 207
QY 277 IKQVYADGQGFELSPIYHVAAIDIFLKAYSARKVLEKEFPQSYVOTVENMIMA----- 332
Db 208 PEKVFTEGVHKEHSPSYHL-----LVASNIKKLANMKBFDRKE-VSLIFENKIYKITEE 260
QY 333 -LISISLPDYNTMPFGDSW--ITDKNFRMAQFASWARVFPANQAIKYFATDGKOGKAPNF 389
Db 261 YAIHIRPDGSLPICDTEANLVGNKY-----DLYESDQVL-VYVTKGKGKAPTE 311
QY 390 LSKALSAGFTYFRSGWDK--NATVMVLKASPPGEPHQAQPDNGTFELFKGRNFTPDAGV 447
Db 312 DDKVFPKSGVAIFRNDWSKEEKATYVLFPTAAHYVDYKHSD-----DLNL 356
QY 448 FVYSGDEALMKL--RNWYR-----QPIHSTLTLIDNQNWITKARQNK-----WET 491
Db 357 IYISNGEILITAGNGYNYKDPFTEYAYSFAHNTLIVDGKGLPRTDRQYKLVLSYDI 416
QY 492 GNLDVLTYTNPSYPLNDHORSVLFINKKYPLVT--DRAIGBATGNLGVHOLKEDSNPVE 550
Db 417 NKDKVEATGYNLRTGVVHSESTVSYMKDEKIVVDLVKSDKREYKLLMHWASD---IT 473
QY 551 DTKNRYVITYRDGNLMIOSL-----NADRTSLNEE--EGKVSYYNNKELKRPAPVFEKPK 605
Db 474 VHVDRDRIVELFRNNHKVMEMEVTTVTGVSIRALNEQTKPQS-----GWVFPKMG 523
QY 606 KNAQTQNFVSIVYPYDQKAPESIRENKGNDFEKK-----LNLITLTINGKQOL 655
Db 524 EKRGK---TIEVDISGSNVE--CITEFRUKDFKLGKRDLLIPNLEKTFKSTRNL 573
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## RESULT 2

```
US-10-282-122A-71561
; Sequence 71561, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
```

```
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 71561
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Staphylococcus haemolyticus
US-10-282-122A-71561

Query Match
Best Local Similarity 3.7%; Score 130.5; DB 12; Length 681;
Matches 134; Conservative 88; Mismatches 256; Indels 193; Gaps 27;

QY 9 IIVFAVIALSGNI-LAOSSSIITKDFDHNLEYSGLEK-----VNKAVAGN----- 55
Db 30 VWIFGIIVRLGYLQIAQS-----QYSQLVKNDENTVNESVPRGRILDRNG 77
QY 56 ---YDDAAKALLAYREKSKAREPDFSNAPKPAD--IRQPIDKVT----- 96
Db 78 KVLVDNASKLITTYTRSRKTSQKMDLTAKLSLITMKTDKITERKQDFWIKHQDEV 137
QY 97 -----EMADKALVHQFQPHKG-----YGYFDYKGINWQ 125
Db 138 DKLMKKEITMLNEGSITQDOYDKLYKKVGDKQINSLSKKDLRLVALYREMSAGSTWNPQ 197
QY 126 MWPKVQNEVRWQLHRVKWQAMALVHATGDEKYAREWVYQYSDWARKNPLGLSQDNDF 185
Db 198 --TKNEDVSEK-----EYAAVSQQLDSLPGVNTMDWDRYPYV----- 235
QY 186 VWRPLEVSDRVQSLPPTFSFLVNSPAPTPAFLEFLNSYHQADYLSHYAEQGNHRLFE 245
Db 236 -----DTLRSI---FGSVSTSSSEGI PKELTE-----QYLAKGYS----- 266
QY 246 AQNLFAVGSFPE--FKDSPRWQTGI-----SVLNTE--IKQVYADGQMFELSPIY 294
Db 267 --RNDRVKSYLEYQYEDILRGKKEMKYTTDKSGKVINSEVINPGSRGDDLQI----- 318
QY 295 HVAADIFLKAYSARKVN--LEKEFPQSYVQVTENNIMALISLSDYNTPEGDSWIT 352
Db 319 ---TIDIDLO---KKVESLLENQIKLRSQAKOMDNALI VQPNKNGDIILAMAGKQI 370
QY 353 DKNFRMAQF--ASWARVFPANQAIK-----YFATDGKQKAPNLFSLKALSAGFTYFR 403
Db 371 DKNGKLTDDYDLGNFTGQFAVGSVSKGTLLAGYQNNAIKVGE--EMIDEPLHFKGGLTKR 428
QY 404 SGWDKATVMVLKASPPGEPHQAQPDNGTFELFKGRNFTPDAGVFTVSG-----DBAI 456
Db 429 SYFNKNDKVR-----NDKEALMHSSNVYMF---KTALKLAGDPYYSGMGLPTDISEAG 479
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Qy      457 MCLRNYWYOTRIHSTLTLDNQNMVITKARONKWETGNLNDLVITYNPFSPYNLDHORSVLF 516  
Db      480 QKLRLGLNVQLGVKTGIDLNETTGQLEPLNNNGNYLDLSIGQVDVTYPQLSQYST    539  
  
Qy      517 INKKYFLV---IDRAIGEATGNLGHWQJLKEDSNPVEDTKNRVVTTYTDGGNNLMIQSLN 573  
Db      540 IANDGYRTQPQHIGHLAHDATNS-----DDIGPVKQIKIGNVLNKVNSEDEIKEVOK 591  
  
Qy      574 ADRTSINEEG   584  
Db      592 GFEMAFNEKDQ   602
```

RESULT 3  
US-09-802-285-3  
Sequence 3, Application US/09802285  
Patent No. US20020122793A1  
GENERAL INFORMATION:  
APPLICANT: Liu, Dongfang  
APPLICANT: Pojasek, Kevin  
APPLICANT: Shriver, Zachary  
APPLICANT: Holley, Kristine  
APPLICANT: El-Shabrawi, Yosuf  
APPLICANT: Venkataraman, Ganesh  
APPLICANT: Sasisekharan, Ram  
TITLE OF INVENTION: Heparinase III and Uses Thereof  
FILE REFERENCE: M0656/7063HCL  
CURRENT APPLICATION NUMBER: US/09/802,285  
CURRENT FILING DATE: 2001-03-08  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 3  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Flavobacterium heparinum

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Query Match      3.7%; Score 128; DB 9; Length 25;
Best Local Similarity 100.0%; Pred.No. 0.00011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

RESULT 4
US-10-291-337-3
; Sequence 3, Application US/10291337
; Publication No. US20030099628A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Dongfang
; APPLICANT: Pojasek, Kevin
; APPLICANT: Shriver, Zachary
; APPLICANT: Holley, Kristine
; APPLICANT: El-Shabrawi, Yosuf
; APPLICANT: Venkataraman, Ganesh
; APPLICANT: Sasisekharan, Ram
; TITLE OF INVENTION: Heparinase III and Uses Thereof
; FILE REFERENCE: M0656/7063HCL
; CURRENT APPLICATION NUMBER: US/10/291.337
; CURRENT FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Flavobacterium heparinum
US-10-291-337-3

```

Query Match	3.7%;	Score 128;	DB 14;	Length 25;
Best Local Similarity	100.0%;	Pred. No. 0.00011;		

	Matches	25;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	280	QVYADGMQFELSPTIYHVA	DI	ELK	304					
Db	1	QVYADGMQFELSPTIYHVA	DI	ELK	25					

RESULT 5  
 US-10-282-122A-70746  
 ; Sequence 70746, Application US/10282122A  
 ; Publication No. US20040029129A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Liangsu  
 ; APPLICANT: Zamudio, Carlos  
 ; APPLICANT: Malone, Cheryl  
 ; APPLICANT: Haselbeck, Robert  
 ; APPLICANT: Ohlsen, Kari  
 ; APPLICANT: Zyskind, Judith  
 ; APPLICANT: Wall, Daniel  
 ; APPLICANT: Trawick, John  
 ; APPLICANT: Carr, Grant  
 ; APPLICANT: Yamamoto, Robert  
 ; APPLICANT: Forsyth, R.  
 ; APPLICANT: Xu, H.  
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 ; FILE REFERENCE: ELITRA.034A  
 ; CURRENT APPLICATION NUMBER: US/10/282,122A  
 ; CURRENT FILING DATE: 2003-02-20  
 ; PRIOR APPLICATION NUMBER: 60/191,078  
 ; PRIOR FILING DATE: 2000-03-21  
 ; PRIOR APPLICATION NUMBER: 60/206,848  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 60/207,727  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/230,335  
 ; PRIOR FILING DATE: 2000-09-06  
 ; PRIOR APPLICATION NUMBER: 60/230,347  
 ; PRIOR FILING DATE: 2000-09-09  
 ; PRIOR APPLICATION NUMBER: 60/242,578  
 ; PRIOR FILING DATE: 2000-10-23  
 ; PRIOR APPLICATION NUMBER: 60/253,625  
 ; PRIOR FILING DATE: 2000-11-27  
 ; PRIOR APPLICATION NUMBER: 60/257,931  
 ; PRIOR FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: 60/267,636  
 ; PRIOR FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: 60/269,308  
 ; PRIOR FILING DATE: 2001-02-16  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 78614  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 70746  
 ; LENGTH: 696  
 ; TYPE: PRT  
 ; ORGANISM: Staphylococcus epidermidis  
 US-10-282-122A-70746

Query Match	3.6%	Score 126.5;	DB 12;	Length 696;
Best Local Similarity	18.6%;	Pred. No. 0.026;		
Matches 139;	Conservative 109;	Mismatches 284;	Indels 217;	Gaps 31;
QY	9	IIIVAVIALSSGNI-LAQSSSITR--KDFHINLEYSLEKVKVAAGN-----Y	56	
Db	30	VFIIVVLRUGYQIIAQSGHYKLIKNENIT-----VNESVPRGILDRNGKVLV	81	
QY	57	DDAAKALIAVYREKSKAREPDFSNAEKPAD-IROPIDKVTREMAADKALVHQPQHKGYGY	115	
Db	82	DNASKWMSITYTRNKTSQKEMLNTAKKLTDLIKMDDKITER--DK-----	125	
QY	116	FDYGGKDNQWMP-----VKONEVRKQLHRV--KWKQA	146	
Db	126	----KDFWIQWYPPSSAKKLARKEQLMLEDGSIISODQFDTLDRKIGKKQLKQFKTDLQV	181	

147 MALV-----YHATGDEKAYAREWVYQYSDWARKNPLGLSQDND 183  
182 LAIYREMNAGSTLDPQTIKNEVDSEKAYAAVSQSLKPLPGVNTTMDWDRKPYG---DTL 238  
184 KFWRPLEVSROVSLPPTFSLFVNSPAFTAFMEFLNSVHQADYLSTHYAQQNHLR 243  
239 RGIFG--DVSTSTGIPKELT-----EQYLSKGYSRNDRVGKSYLEYQVEDV 283  
244 FEARNLPAVGFPEFKDPSRWQRTGISVLNTEIKQVYADGMQFELSPIYHVAIDIFL 303  
284 LKGTQKQ-----KYTTDKSGRVISSEVLNPGSR-----GHDQLQUT-----IDIDL 324  
304 KAYGSAKRVN--LEKEFPQSVQTVENMIMALISISLPDYNTPMFGDSWITDKNFRMAQF 361  
325 Q-----KKVESLLEKQISKLRSQAKMDNALMVVNQPNKGDILAIAGKQIDKQKLUKY 379  
362 --ASWARVFPANQAIK-YFATDGKQKAPN-----FLSKALSNAGFYFPRSGWDKNA----- 410  
380 DIGNFTAQYTVGSSVKGGTLLAGYQNKAINVGETWVDEFLKFGGGLTKRSYFNKNHVS 439  
411 -----TVMVLKAPPGFEHQAQPDNGTFELFIKGRNFTPDAGVFVYSGDE 454  
440 DDQALMHSSNVYMEKALAGDPYTSGMSLPNN-----IADAG----- 479  
455 AIMKLNRWYRTRIHSTLTLDNQNNVITKARQNKWETGNNLDVLTYNPSYPNLDHORSV 514  
480 --RKLKGLNQVGLKGTIDLPNETPGQIEPLTNPNNGYLDLAIQYDVTYTPQLSQYV 537  
515 LFINKKFLV---IDRAIGBATNGLGVHWQKESNVPDFKTRVYTYRDNLMQIS 571  
538 STIANDGRIOPHIGLSIYESTN-----KDETGPLKRIKGNVLNKNVNSNDEIKEV 589  
572 LNAURTSINEEGKVSYYVYNKELKRP-----AFVEE--KPKKNAGTQNFVSVIYP--- 619  
590 QEGFKMAFNEKQG--TGVASFRNTVPSAGKTGTAEVFDQGEPRVNSYIYIAPVDDPKLS 648  
620 ----YDGKQKAPESIRENKNKGNDFEKGKLN 644  
649 FSIYVYTNQVPVPPWL---NGGDLGRDVIN 674

RESULT 6  
US-10-369-493-22074  
; Sequence 22074, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; PRIOR FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 22074  
; LENGTH: 532  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-10-369-493-22074

Query Match 3.5%; Score 123; DB 15; Length 532;  
Best Local Similarity 18.9%; Pred. No. 0.035;  
Matches 109; Conservative 76; Mismatches 179; Indels 214; Gaps 31;  
94 VTREMAKALVHQFQPHKGY-----GYFDYKQINQWQW-PVKDNEVRWQLHRVKKWQAM 147  
21 MTNETSDRPLVH-FTPNKGWMDNGLWYDEKAKWLYFYQNPNDIVW--GTFPLFWG-- 75

148 ALVYHATGDEKAYAREWVYQYSDWARKNPLGLSQDNDKFWRPLEVSDRVQSLPPTFSLFV 207  
76 ---HATSD-----LTNW-EDQPIAIAPRN----- 97  
208 NSPAFTPAFLMEF-----LNSYHQOADYLSTHYAQQNHLRFE 245  
98 DSGAFSGMVVDYNTSGFNDTIDPRQCVAIWYNTPESEEQVIS--YSLDGGYTTFE 155  
246 AORNLPAGVFPPEFKD-----SPRWQRTGISVLNTEIKQVYAD----- 284  
156 YQNPVLAANSTQPRDPKVPFWYEPESQKWMT--AAKSQDYKIETIYSSDDLKSWKLESAPA 213  
285 -----GMQFEL-----SPIYHVAIDI-----FLKAY 306  
214 NEGLGVQYCEPGLIEVPTQDPSKSYWVMEISINPGAPAGGSNQYFVGSFNGTHFAP 273  
307 GSAKRVNLEKEFPQSV--VQTVENMIMALISISLPDYNTPMFGDSWITDKNFRMAQFA-- 362  
274 DNQSRV---VDFGKDYVALQTFEN-----TDPTYGSAL-GIAWAS--NWEYSAFVPT 319  
363 -----SWARVFPANQAIKYFA--TDGKQKAPNLSKALSNAAGFYFPRSGWDKNAIV 412  
320 NPMRSSLSVRKFSLN--TEYQANPETELINLKAEPILN--ISNAG-----PWSRFATN 369  
413 MVLKASPPGFEHQAQPDNGTFELFIKGRNFTPDAGVFVYSGDEAIAK-----LRNWIQTR 467  
370 TLTKANSYNDLSNSTGTLEFEL-----VYAVNTTQTTISKSVFADLSLWFKGLE 419  
468 -----IHSTLTLDNQNNVITKARQNKWETG-----NNLDVLTYNPSYPN----- 507  
420 DPEYLRMGFEVSASSFFLDGRNSKVFVKENPYFTNRMSVNNQPFKSENDLSYKYVGL 479  
508 LDHORSVLFN-----KKYELVIDRAIGBATNGLGV 538  
480 LDQNILEYDNGDVSTNTYFMTTGNALGSVNNMTGV 517

RESULT 7  
US-10-369-493-23212  
; Sequence 23212, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 23212  
; LENGTH: 677  
; TYPE: PRT  
; ORGANISM: Bacillus subtilis  
US-10-369-493-23212

Query Match 3.4%; Score 120; DB 15; Length 677;  
Best Local Similarity 18.8%; Pred. No. 0.097;  
Matches 123; Conservative 83; Mismatches 216; Indels 232; Gaps 32;  
41 YSGLEKVNKAVAGNVDAAKALLAY---REKSKAREPDEFSNAEKPADIRQPIDKVTRE 97  
105 FSGSVVDKNTTSGFQTKGKPLVLIYTDQREGHQVQSIAYSNDK-----GRTWTK 155  
98 MADKALVHQFQPHKGYFDYDGDINQWMPVKDNEVRWQLHRVKKWQAMA-----LVYH 152  
156 YAGNPVI-----PNPG-----RDPKVFWEYKEKKWVWVLAAGDRILIY- 197

QY 153 ATGDEKAYREWVYQYSDWARKNPLGLSDNDKFWVRPLEVSDVQSLPPTFSLFVNSPAF 212  
DB 198 ---TSKNLKWITY-----ASEFGODQGHGVM-----ECPDLFELPVDGNPN 237  
QY 213 TPAFLMEF-----LNSVHQQADYLSTHYAEOG--NHRLF-EAQRNLFAGVSFPPEF 259  
DB 238 OKKWVQVGVNGVAGVSGGGMQYFVGDFGTHFKNENPENKVLWTDYGRDFVAAVSWSDI 297  
QY 260 --KDSR-----WRQTGSLVLTTEIKQVYADGMQFELSPIYHVA 298  
DB 298 PSTDSRLMLGWSNWOYANDVPTSPWRS--TSIPRELKKAFTAGVVRVQTPVKELET 355  
QY 299 I-----DIFLKAYGSAKRVNLE-KEFPQS-----YYQTVENMIM--- 331  
DB 356 IRGTSKKKNLITSPASHVNLGQSGDAVEINAEFKVSPGSAABFGFKVYRTGENQTKVG 415  
QY 332 ----ALISISLPDYNTPMFGDSWIITDKN---FRMAQFASWARVFPANQAIKYFATDGKQ 383  
DB 416 YDRNAKLFVDRSESGNDTFNPAFTGKETAPLKPVNGVKVLRIFVDRSSVEVFGNDGKQ 475  
QY 384 GKA----PNFLSKAL-----SNAG-----FYTRSGWMDKKNATVMVLK 416  
DB 476 VITDIILPDRSGKGLYAAANGVKVKSITIHLKKVWGTTPTFMSNMTCW---TTV----- 528  
QY 417 ASPPGEFHAQPNGTPELFIKGRNFTPDAGVFVVS-----GDEA 455  
DB 529 -----NGTWADTIEGKQSGDGSFLLSSASGSDFTYBESDIITKONGRGAGA 576  
QY 456 IMKLRNWRQTRIHSITLDNQNMVITKARQNKWETGNNLDVLTYPNPNLDHQRSVL 515  
DB 577 LM-----FRSDKDNKGYLANVDAKHLVKFPKFGNGAASVIAEYKTP-----I 620  
QY 516 FINKKYFL-----VIDRAIGEA-----TGNI/GVH-WQKEDSNPVF 550  
DB 621 DVNKKYHLKTEABGRFKIYLDRLVIDAHDVSFSEGFGLNVW-----DATAVF 670

RESULT 8  
US-10-369-493-2315  
; Sequence 2315, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 2315  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Schizosaccharomyces pombe  
US-10-369-493-2315

Query Match 3.4%; Score 118.5; DB 15; Length 579;  
Best Local Similarity 20.9%; Pred. No. 0.11;  
Matches 111; Conservative 75; Mismatches 195; Indels 151; Gaps 31;

QY 112 GYGFDYGDKNQWMPVKD-NEVRWQLHRVKKWQAMALVYHATGDEKYAREWVYQYSDW 170  
DB 70 GYDVSDY-KQIDSRYGTLDELRLMKALHERDMKLVMDLVNHTSDQ---HEW-FKESRS 124

QY 171 ARKNPLGLSDNDKFWVRPLEVSDVQSLPPTFSLFVNSPAFTPAFLMEFLNSYHQADY 230  
DB 125 SKTNP-----KRDWYFKWPARYNEKGERLPP-----NNWRSYFDT 159

QY 231 LSTHYAEOGNHRLFAQRNLFAGVSFPPEK-DSPRWQRTGISVLNTEIKQVYADGMQFE 289  
DB 160 SAWEDEATQ-----EYLLHLS-VGQPDNLNWTTPKVRVAVHDLIRFWLDRGV--DG--PR 210  
QY 290 LSPYHVAADIFLKA-----YGSARVNLEKEFPQSYQTVENMIMALI 334  
DB 211 LDAINWISKDQRFLOAPITDDRYEYQLAYQYANGPRIH-----EYLANGIGNI----- 258  
QY 335 SISLDPYNTMFGD-SWITDKN-----FRMAQFASWARVFPANQAIKYFATD 380  
DB 259 ---LTEYDAFSGEMPYVLDITNEILHVVGADRRELTMIQDFDVLDDLPNQH-KYIEGS 314  
QY 381 GKQKAPNFLSK---ALSNAGF-YTRSGWMDKKNATV-MVLKASPPGEPHQAQPDNGTREL 434  
DB 315 WELSDKLKSLKQWQALLSGGNNASFIEHDDQTRTVSRYLSDSPKRYRAYSKLMALFII 374  
QY 435 FTKGRNFTPDAGVFVYSGDEAIMKLRNWRQTRIHSITLDNQNMVITKARQNKWETGNN 494  
DB 375 FQSG---TP---FVFQGE---LALANIPRDWPIDEYLDVETQNF-----WK--- 412  
QY 495 LDVLYTTPSNYLNLDHQRSVLFINKKYFLVIDRAIGEAATGNLGVHQLKEDSNPVEDTK 554  
DB 413 --LFMSGNPSQEEI--EKTMDIVNKR-----ARDNGRTPMEHW---DSSPENGFTK 455  
QY 555 -----NRVYTTYRDGNNLMIQSLNADRTSLNEEGKVSY-----VYNKELK 595  
DB 456 AGVKPMWRVTNDYKEWN-----AANQVNDPSPYTFWSKALELRKELK 498

RESULT 9  
US-10-369-493-2321  
; Sequence 2321, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 2321  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Schizosaccharomyces pombe  
US-10-369-493-2321

Query Match 3.4%; Score 118.5; DB 15; Length 579;  
Best Local Similarity 20.9%; Pred. No. 0.11;  
Matches 111; Conservative 75; Mismatches 195; Indels 151; Gaps 31;

QY 112 GYGFDYGDKNQWMPVKD-NEVRWQLHRVKKWQAMALVYHATGDEKYAREWVYQYSDW 170  
DB 70 GYDVSDY-KQIDSRYGTLDELRLMKALHERDMKLVMDLVNHTSDQ---HEW-FKESRS 124

QY 171 ARKNPLGLSDNDKFWVRPLEVSDVQSLPPTFSLFVNSPAFTPAFLMEFLNSYHQADY 230  
DB 125 SKTNP-----KRDWYFKWPARYNEKGERLPP-----NNWRSYFDT 159

QY 231 LSTHYAEOGNHRLFAQRNLFAGVSFPPEK-DSPRWQRTGISVLNTEIKQVYADGMQFE 289  
DB 160 SAWEDEATQ-----EYLLHLS-VGQPDNLNWTTPKVRVAVHDLIRFWLDRGV--DG--PR 210  
QY 290 LSPYHVAADIFLKA-----YGSARVNLEKEFPQSYQTVENMIMALI 334  
DB 211 LDAINWISKDQRFLOAPITDDRYEYQLAYQYANGPRIH-----EYLANGIGNI----- 258





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; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70737
; LENGTH: 919
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-70737

Query Match      3.3%; Score 116; DB 12; Length 919;
Best Local Similarity 18.2%; Pred. No. 0.37;
Matches 124; Conservative 84; Mismatches 216; Indels 258; Gaps 31;

Qy 56 YDDAAKALLAYREKSKAREPDFSNAEKPADIR-----QPIDKVTREMADK 101
Db 370 YDKANKAVTLLKEDKALLKDLFTHSYPHDWRTKKVI PRATQWFSINKVRQDILDA 429
Qy 102 ALVHQFQPHKGYGFDYCKDINQMWPVQKONEVWQLHRVQWQAMALVYHA-TGDEKYA 160
Db 430 IEDTNFK-----VDMGKTRIYN--IRDRG-EWVISRQVWGVPLPVFAENGDIIMT 479
Qy 161 REMVYQYSDWARKNPLGLSQDNDFVWRPLEVSRVQSLPTTSLFVNSPFTAFLEMEF 220
Db 480 KETVNHVAD-----LFEKHGNSINWFRKEAK---ELLPEGFS-HFGSPN----- 518
Qy 221 LNSYHQQADYLSTHYAQGNHR-LFEAQRLNLFAGVSFPE---PKDSPRWRGTGISVLNTE 276
Db 519 -GEFTKETDMDVWFDSGSSHRGVLETRPEL-----SEPADLYFGSQOYR---GWNFS 569
Qy 277 IKQVYADGQMFELSPIYHVAIDIFLKAYGSAKRVNLEKEFPQSYQVTVENMIMALISI 336
Db 570 ITTAVATRGQ-----APYKFLLSHG----- 589
Qy 337 SLPDYNTPMFGDSWITDKNFRMAQFASWARVFPANOAIKYFATDYGKQKQKAPNLSKALSN 396

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Db 590 -----FVMDG-EGKK-----MSKSLGN 605
Qy 397 AGFYFRSGWCKNATVMVLKASPPGEFHAQPDNGTFFELFIKGRNFTPDAGVVFVSGDEAI 456
Db 606 -----VIV-----PDQVVKQKADIAFLWVSSDYLSDVRI-----SDEIL 641
Qy 457 MCLRNNWYQTR-----IHSTLTLDNQNMWITKARONKWKETNNLDV 497
Db 642 KQTSDEVYRKENTLRFMLGNINDFNPDTSIAETNLLVEDRYLLNRLREFTASTINNEN 701
Qy 498 LTYTN-----PSYPN-----LDQRSVLFINCK-----YFLVIDRAIGBAT 533
Db 702 FDYLNLYQEVQNFVNSLNFYLDYKDLVIEKKSHKRSMTVLVYQILVD--MTKLL 759
Qy 534 GNLGVH-----W-----OLKEDSNVFDKTKY-----RVYTYRDGNLMIQSLN 573
Db 760 APILVHTAEVWMSHTPHVKEESVHLSDMPKVVVDDEELLEKKWNTFMNLRDDVNRALQAR 819
Qy 574 ADRTSLNEEGKVSIVYNKELKRPAPVFE-----KPKKNAGTQNFVSIVY 618
Db 820 NEKVIGKSLEAKVVGSGNESFNTAEFLQOQFNDLQQLFIVSQVEYKDKVNDG-----VSY 873
Qy 619 PYDQKKAPEISIRENKGNDFEK 640
Db 874 QYG-----DIHIKHAEGEKCEK 890

RESULT 14
US-09-802-640-32
; Sequence 32, Application US/09802640
; Publication No. US20030036057A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bonsal Aruna
; APPLICANT: Kieyn Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
; FILE REFERENCE: 24736-2048
; CURRENT APPLICATION NUMBER: US/09/802,640
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 4563
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-802-640-32

Query Match      3.3%; Score 116; DB 10; Length 4563;
Best Local Similarity 16.3%; Pred. No. 4.4;
Matches 104; Conservative
Qy 218 MEFINSY-----HQADY-----LSTHYAEOGNHRLFEA-----QBNL----- 250
Db 3068 IDFLNNYALFLSPSAQOASQVSAFENQYKYNQNFSAQNNENIMEAHVINGEANGLDPLN 3127
Qy 251 -----FAGVSPEEKDSPRWEQTG----- 269
Db 3128 IPLTIPMRPLPYITITTPPLKDFSLWBEKTLGKLEKTKTKQSFDSLVSQAQYKKNKHSIT 3187
Qy 270 --ISVLNTEIKQVYADGQMFELSPIYHVAIDIFLKAYGSAK-----RVNLEK---BFPQ 320
Db 3188 NPLAVLCEFTISQSISFDRHFEKN--RNNALDPVTKSYNETKIKFDKYKAERKSHDELPR 3244
Qy 321 SYQVTVENMIMALISLSPDYNTPMFGDSWITDKNFRMAQF-----ASWARVFPANOAIKY 376
Db 3245 TF-----QIPGYTPVV-----NVEVSFPTIEMSAFGVYFVFPKAVSMPS 3282
Qy 377 FATDYGKQKAPNF-----LSKALSNAGF-YT 401
Db 3283 FSLIGDSVRVPSVTLLPLSLVPLVHVPRLKLSLPHKELCTLSHTIFIPAMGNITVDFS 3342
Qy 402 FRSGWCKNATVMVLKASPPGEFHAQPDNGTFFELFIKGRNFTPDAGVVFVSGDEAI----- 456

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Db 3343 FKSS-----VITLNTNLEFNQSD--IVAHLSSSSVVDALQYKLEGTTLTRKRG 3392  
QY 457 -----MKLRNWRQTRIHTSLTDNQNMVITKARQNKWE-----TGNLNDVL 498  
Db 3393 LKALATLSLNKFEVSHNSTVSLTTKNMEVSVAKTTKABIPILRMNFKQELNGNTKSKP 3452  
QY 499 TYTNPSYPNLDHORSVLFINKK-----YFLVIDRAIGEAATGNL----- 536  
Db 3453 TVSSSEFFKDFNSMLYSTAKGAVDHKJLSLESLTSYFSIESSTKGDVKGVSLSRBSYSGT 3512  
QY 537 -----GVH-----WOLKEDSNPVPDKTKNRVYTYTYRDG--NNLM 568  
Db 3513 IASEANTYLNKSTRSSVKLQGTSKIDDINWLEVKENFAGEATLQRIYLSWEHSTKNHLQ 3572  
QY 569 IQSL-----NADRTS---LNEEGKVSYYNKKELKRPAPVFEKP-----KKNACTON----- 612  
Db 3573 LEGLFTNGEHTSKATLELSPWQMSALVQVHASQPSSEHDFPDLGQBEVALNANTKNQKIR 3632  
QY 613 FVSIVVYPDQKAPETISIRENKGNDEPKGLNLTTLTING 651  
Db 3633 WKNEVRIHGSFOSQVEL-----SNDQEKALHDITAGSLLEG 3667

## RESULT 15

US-10-282-122A-48445  
; Sequence 48445, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 48445  
; LENGTH: 987  
; TYPE: PRT  
; ORGANISM: Bacteroides fragilis  
US-10-282-122A-48445

Query Match 3.3%; Score 115.5; DB 12; Length 987;  
Best Local Similarity 19.1%; Pred. No. 0.46;  
Matches 105; Conservative 79; Mismatches 188; Indels 179; Gaps 24;  
QY 11 VFVAIALSSGNILAQSSSITRKDFDHINLEYSGLEKVNKA-----VAAGNYDDAAKALL 64  
Db 282 VFSKAAETLGEVTTESDAUTQNALYHMLGLAYLHLAEKNKARMAFEQAASANLKIKEQA 341  
QY 65 AY-----YREKSKAREP---DFSNAE-----KPA 85  
Db 342 AYNVALCIHETSYSARGESVTVFEKFLNEFPNSEYAEWSSYLVEYVMNTRSYEAALKSI 401  
QY 86 D-----IRPIDIKVTREMAKALVH-QFQPHKGYGYFDYKQKINWQMPVKDNEVRW 136  
Db 402 DRIAHPGKRILEAKQRIPLQGTQAFANTQFE--QAIGYFDRSLGLGQYNROTQADALYW 459  
QY 137 -----QLHRVKWQWQAWALVYHATGDEKYAREWVYQYSDWARKN 174  
Db 460 RGEAYYRLNRMEEAKNFTDYLOLTQOTNEMVALAHYINLGYIAFHQKDYTOQNWFRK- 518  
QY 175 PLGLSQDNDFVWRPLEVSDRVQSLPPTFS---LFVNSPAPFTPAFLMEFLNSYHQADY 230  
Db 519 -----YISLEKGENKTALADAYNRIGDCYLDVRNFDEA-----KHYYSQAEA 560  
QY 231 LSTHYAEQGNHRLFE-----AORNLPAGVSFPFEPKDSPRMOTGIGSVLNT 275  
Db 561 MNT---PSGDYSFYQLALVSLGQKDYSGKITLINRLAG---KYPASP---YAISALYE 609  
QY 276 EIKKQVYADGMO-----FELSPYHVAADIELKAYGSA---KRVNLEKEFPQ 320  
Db 610 KGRSYVLMNNOQAIASTFKELLAKYPESPVSXKAAAEIGLLYYQNEEDYDOAINAYKQVVQ 669  
QY 321 SYVQTVENMIMALISITSLPDYNTPMFGDSWITDKNFRMAQAFASWARVFPAN-----Q 372  
Db 670 KYPGSD-----ARLAMEDLK-----SIYVDMN-RIDEFAALASAMEGNIFFDASEQD 716  
QY 373 AIKYFATD-----GKQKAPNFLSKALS-----NAGFYTFRSGWKNATVMVYLKAS 418  
Db 717 SLTYMAAEKIYIRGRVEQAKESFGKYLQTFPDGAFGLNAHYLCLIGKEQKNYDMILEHS 776  
QY 419 PGCEFHQAQPDN 429  
Db 777 --GKLLLEYPD 785

Search completed: March 18, 2004, 04:13:39  
Job time : 48 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 28, 2003, 20:48:13 ; Search time 29 Seconds  
(without alignments)  
961.478 Million cell updates/sec

Title: US-09-802-285A-2

Perfect score: 3494

Sequence: 1 MTTKFKRIIVFAVIALSSG.....KGLNLTITNGKQLVLVP 659

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgm2\_6/ptodata/1/iaa/5A-COMB.pep:\*  
2: /cgm2\_6/ptodata/1/iaa/5B-COMB.pep:\*  
3: /cgm2\_6/ptodata/1/iaa/6A-COMB.pep:\*  
4: /cgm2\_6/ptodata/1/iaa/6B-COMB.pep:\*  
5: /cgm2\_6/ptodata/1/iaa/PCTUS-COMB.pep:\*  
6: /cgm2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3494	100.0	659	1	US-08-258-639A-4	Sequence 4, Appli
2	3494	100.0	659	2	US-08-900-951-4	Sequence 4, Appli
3	3494	100.0	659	5	PCT-US95-07391A-4	Sequence 4, Appli
4	126.5	3.6	698	4	US-09-134-001C-3632	Sequence 3632, Ap
5	124	3.5	23	1	US-08-258-639A-9	Sequence 9, Appli
6	124	3.5	23	2	US-08-900-951-9	Sequence 9, Appli
7	124	3.5	23	5	PCT-US95-07391A-9	Sequence 9, Appli
8	119	3.4	23	1	US-08-258-639A-10	Sequence 10, Appl
9	119	3.4	23	2	US-08-900-951-10	Sequence 10, Appl
10	119	3.4	23	5	PCT-US95-07391A-10	Sequence 10, Appl
11	119	3.4	1138	1	US-07-973-320-2	Sequence 2, Appli
12	119	3.4	1138	1	US-07-973-320-4	Sequence 4, Appli
13	118	3.4	772	1	US-08-258-639A-2	Sequence 2, Appli
14	118	3.4	772	2	US-08-900-951-2	Sequence 2, Appli
15	118	3.4	772	5	PCT-US95-07391A-2	Sequence 2, Appli
16	116	3.3	4536	4	US-09-180-422B-27	Sequence 27, Appl
17	115.5	3.3	1168	1	US-08-620-717A-9	Sequence 9, Appli
18	114.5	3.3	1167	1	US-08-485-568A-6	Sequence 6, Appli
19	114.5	3.3	1167	2	US-08-590-554A-6	Sequence 6, Appli
20	114.5	3.3	1167	2	US-09-184-223-6	Sequence 6, Appli
21	113.5	3.2	1398	1	US-08-750-532-9	Sequence 9, Appli
22	113.5	3.2	1398	3	US-08-894-818B-8	Sequence 8, Appli
23	113.5	3.2	1398	4	US-09-445-472-6	Sequence 6, Appli
24	111	3.2	927	4	US-09-134-001C-4831	Sequence 4831, Ap
25	110	3.1	4563	4	US-09-108-006C-1	Sequence 1, Appli
26	109	3.1	951	3	US-08-816-346-58	Sequence 58, Appl
27	109	3.1	951	3	US-09-335-411-58	Sequence 58, Appl

28 109 3.1 952 2 US-08-788-674-5 Sequence 5, Appli  
29 109 3.1 952 3 US-08-816-346-4 Sequence 4, Appli  
30 109 3.1 952 3 US-09-335-411-4 Sequence 4, Appli  
31 106 3.0 884 4 US-09-328-352-4598 Sequence 4598, Ap  
32 106 3.0 945 4 US-09-198-452A-1030 Sequence 1030, Ap  
33 106 3.0 1375 3 US-09-210-361-4 Sequence 4, Appli  
34 106 3.0 1375 4 US-09-740-274-4 Sequence 4, Appli  
35 105 3.0 443 4 US-09-328-352-6322 Sequence 6322, Ap  
36 105 3.0 741 4 US-09-252-991A-22440 Sequence 22440, A  
37 105 3.0 965 4 US-09-437-277-3 Sequence 3, Appli  
38 104 3.0 1849 4 US-08-851-567B-49 Sequence 49, Appl  
39 104 3.0 2516 4 US-08-851-567B-47 Sequence 47, Appl  
40 103.5 3.0 1183 2 US-08-447-031A-2 Sequence 2, Appli  
41 103.5 3.0 1338 2 US-08-728-470-9 Sequence 9, Appli  
42 103.5 3.0 1338 3 US-08-719-641-9 Sequence 9, Appli  
43 103.5 3.0 1599 2 US-08-617-697-9 Sequence 9, Appli  
44 103.5 3.0 10182 4 US-09-134-001C-3159 Sequence 3159, Ap  
45 102.5 2.9 618 3 US-09-299-378-4 Sequence 4, Appli

## ALIGNMENTS

## RESULT 1

US-08-258-639A-4

; Sequence 4, Application US/08258639A

; Patent No. 5681733

; GENERAL INFORMATION:

; APPLICANT: Su, Hongsheng

; APPLICANT: Blain, Francoise

; APPLICANT: Bennett, Clark

; APPLICANT: Gu, Kangfu

; APPLICANT: Zimmermann, Joseph

; APPLICANT: Musil, Roy

; TITLE OF INVENTION: Nucleic Acid Sequences And Expression

; TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hale and Dorr

; STREET: 1455 Pennsylvania Avenue, N.W.

; CITY: Washington, D.C.

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/258.639A

; FILING DATE: 10 JUNE 1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Healey, William J.

; REGISTRATION NUMBER: 36,160

; REFERENCE/DOCKET NUMBER: 104385.116

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)942-8400

; TELEFAX: (202)942-8484

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 659 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-258-639A-4

Query Match 100.0%; Score 3494; DB 1; Length 659;

Best Local Similarity 100.0%; Pred. No. 5.8e-308;

Matches 659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 MTTKFKRIIVFAVIALSSGNIQAQSSITRKDFDHINLEYSGLEKVNKAAGNYDDAA 60



APPLICANT: ZIMMERMANN, Joseph  
 TITLE OF INVENTION: Nucleic Acid Sequences And Expression  
 TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From  
 TITLE OF INVENTION: Flavobacterium heparinum  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hale and Dorr  
 STREET: 1455 Pennsylvania Avenue, N.W.  
 CITY: Washington, D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/07391A  
 FILING DATE: 09-JUNE-1995  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/258,639  
 FILING DATE: 10 JUNE 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BAKER, Hollie L.  
 REGISTRATION NUMBER: 31,321  
 REFERENCE/DOCKET NUMBER: 104385.116PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)942-8400  
 TELEFAX: (202)942-8484  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 659 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US95-07391A-4

Query Match	100.0%;	Score 3494;	DB 5;	Length 659;
Best Local Similarity	100.0%;	Pred. No. 5.8e-308;		
Matches 659;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MTTKIFKRRIIVFAVIALSSGNILAQSSITRKDPDHINLEYSGLEKYNKAUVAAGNYDDAA	60	
Db	1	MTTKIFKRRIIVFAVIALSSGNILAQSSITRKDPDHINLEYSGLEKYNKAUVAAGNYDDAA	60	
QY	61	KALLAYYREKSKAREPDFSNAEKPADIRQPIDKVTREMAKCALVHQFQPHKGYGVDYDGK	120	
Db	61	KALLAYYREKSKAREPDFSNAEKPADIRQPIDKVTREMAKCALVHQFQPHKGYGVDYDGK	120	
QY	121	DINQMWPFKDNVVRWOLHRVKWQAMALVYHATGDEKYAREWYQYSDWARKNPLGLSQ	180	
Db	121	DINQMWPFKDNVVRWOLHRVKWQAMALVYHATGDEKYAREWYQYSDWARKNPLGLSQ	180	
QY	181	DNDKFVWRPLEVSDRVOSLPPTESLFVNSPAFTPAFLMEFLNSYHQADYI.STHYABQGN	240	
Db	181	DNDKFVWRPLEVSDRVOSLPPTESLFVNSPAFTPAFLMEFLNSYHQADYI.STHYABQGN	240	
QY	241	HRLEFAQRNLFAGVSPPEFKDSRPRWRTG;SVLNTETIKKVYADGMQFELSPIYHVAAID	300	
Db	241	HRLEFAQRNLFAGVSPPEFKDSRPRWRTG;SVLNTETIKKVYADGMQFELSPIYHVAAID	300	
QY	301	IFLKAYGSAKRVNLEKEFPQSYVQTVENMIMALLISISLPDNTMPFGDSWITTDKNFRMAQ	360	
Db	301	IFLKAYGSAKRVNLEKEFPQSYVQTVENMIMALLISISLPDNTMPFGDSWITTDKNFRMAQ	360	
QY	361	FASWARVFPANQAIKYFATDGKQKAPNPLSKALSNAGFYTFRRSGWQKNATVMWLKASPP	420	
Db	361	FASWARVFPANQAIKYFATDGKQKAPNPLSKALSNAGFYTFRRSGWQKNATVMWLKASPP	420	
QY	421	GEPHAQPDNGTTFELFIKGRNFTPDAGVFVYSGDEAI.MKLRNWWYQTRIHSHTLTJDNQMV	480	
Db	421	GEPHAQPDNGTTFELFIKGRNFTPDAGVFVYSGDEAI.MKLRNWWYQTRIHSHTLTJDNQMV	480	

```

Qy 481 ITKARQNKWETGNNLDVLTNTNPSYPNLDHORSVLFINKKYFLVIDRAIGATGNLGVHW 540
    |||||
Db 481 ITKARQNKWETGNNLDVLTNTNPSYPNLDHORSVLFINKKYFLVIDRAIGATGNLGVHW 540
    |||||
Qy 541 QLKEDSNPFDKTKNRVYTYTRDGNLMIQSLNADRTSLNEEGKVSYYNKKELKRPAPV 600
    |||||
Db 541 QLKEDSNPFDKTKNRVYTYTRDGNLMIQSLNADRTSLNEEGKVSYYNKKELKRPAPV 600
    |||||
Qy 601 FEKPKKNAGTQNFVSIVPYPDGQKAPISIRENKGNDFEKGKLNLTITNGKQQLVLVP 659
    |||||
Db 601 FEKPKKNAGTQNFVSIVPYPDGQKAPISIRENKGNDFEKGKLNLTITNGKQQLVLVP 659
    |||||

RESULT 4
US-09-134-001C-3632
; Sequence 3632, Application US/09134001C
; Patent NO. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GPC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3632
; LENGTH: 698
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3632

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Query Match	3.6%;	Score 126.5;	DB 4;	Length 698;
Best Local Similarity	18.6%;	Pred. No. 0.013;		
Matches 139;	Conservative 109;	Mismatches 284;	Indels 217;	Gaps 31;

  

Qy	9	IIVFAVIALSSGNI-LAQSISITR--KDPDHINLEYSGLKYNKAVAAGN-----Y	56
Db	32	VFIFAIVLRLGLYQAQSHYKQLIKNDENIT-   : :	83
Qy	57	DAAKALLAYREKSKAREPDFSNAEKPAD-IRQPIDKVTREMAADKALVHQFQPHKGyGY	115
Db	84	DNASKMSIITYRNKRTKSQKEMLNTAKLITLTKMDTDKITER--DK-----	127
Qy	116	FDYQKIDNNQWMP-----VKDNEVRWQLHRV--KWWQA	146
Db	128	---KDFWIQMPSPFAKMLRKEQLMLEDGSIQQDFTQLRDKICKKQLKQTKDLOV	183
Qy	147	MALV-----YHATGDEKYAREWVQYSDWARKNPLGLSQDND	183
Db	184	LAIYREMNAGSTLDPOTIIRKNEVDSEKYEAAVSQQLKPLFGVNTTMDWRDKYPYG--DRL	240
Qy	184	KFVWRPLEYSDRVQSUPFTFSLFVNSPAFTPAFLMEFLNSYHQQAADYLSHTHVAEQGNHRL	243
Db	241	RGIFG--DVSTSTEGIPKELT-----EQLSKGYSRNRDVGKSLVEYQYEDV	285
Qy	244	FEAQRNLFAGVSPPEPKDSPRWRTQGISVLNTEIKQVYADGMQFELSPIYHVAADIFLT	303
Db	286	LKGTKKQM-----KYTTDKSGRVISSEVLNPGSR-----GHDQLQT-----IDIDL	326
Qy	304	KAYGSAKRNV--LEKEFFPOSYQVTVENMIMALISISLPDYNTPFMFGDSWITDKRNFMAQF	361
Db	327	Q-----KKVESLLEKQISKLRSQGAQMDNALMVQNPKNQDILATAGQIDKQGLKDY	381
Qy	362	--ASWARVFPANAQIK-YFATDGKQKAPN-----FLSKALSNAGFYTFPSGHDKXA----	410
Db	382	DIGNFTAQTVGSSVKGGTLLAGYQNKALNIVGETWYDPELKPQGGITKRESYFNKNGHWSI	441
Qy	411	-----TVMVLKASPPGEPAQPDNGTIFELFKGNFTPDAGVYVYSGDE	454

Db 442 DDQALMHSSNVYMEFKTAGDPTSCMSLPNN-----IADAG----- 481  
QY 455 AIMKLRNRYRQRIHSTITLDNQNWVITKARONKWETGNNLDVLTYPSPYNLDHQRSV 514  
Db 482 --RKLKGLNVLGGLKTGIDLPNETPGQIEPLTNNPGNYLDAIGQYDVTYPLQLSQVV 539  
QY 515 LFINKKYFLV---IDRAEGATGNLGVHWQKEDSNPVFDKTKNRVYTYRDNLMIQS 571  
Db 540 STIANDGRIQPHIGLSIYESTN-----KDETGPLRKRKTKGNVLNKNVNSNDIEKEV 591  
QY 572 LNADETSINEEGKSVYVYNKELRP-----AFVFE--KPKKNAGTQNFVSIYVP--- 619  
Db 592 QEGPKVAFNEKOG-TGYASFRNTVVPVSAGKTGTAEVFDQGEPRVNSTVIGYAPVDDPKLS 650  
QY 620 ----YDGKAPBISIRENKNDPEKGLN 644  
Db 651 FSIYVTNQFPVPPWL---NGGDLGRDVIN 676

## RESULT 5

US-08-258-639A-9  
; Sequence 9, Application US/08258639A  
; Patent No. 5681733  
; GENERAL INFORMATION:  
; APPLICANT: Su, Hongsheng  
; APPLICANT: Blain, Francoise  
; APPLICANT: Bennett, Clark  
; APPLICANT: Gu, Kangfu  
; APPLICANT: Zimmermann, Joseph  
; APPLICANT: Musil, Roy  
; TITLE OF INVENTION: Nucleic Acid Sequences And Expression  
; TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From  
; TITLE OF INVENTION: Flavobacterium heparinum  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington, D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/258,639A  
; FILING DATE: 10 JUNE 1994

CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Healey, William J.  
; REGISTRATION NUMBER: 36,160  
; REFERENCE/DOCKET NUMBER: 104385.116  
; TELEPHONE: (202)942-8400  
; TELEFAX: (202)942-8494  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 23 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-258-639A-9

Query Match 3.5%; Score 124; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 7.9e-05;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 414 VLKASPPGEFFHAQPDNGTGFELFI 436  
Db 1 VLKASPPGEFFHAQPDNGTGFELFI 23

RESULT 6  
US-08-900-951-9  
; Sequence 9, Application US/08900951  
; Patent No. 5919693  
; GENERAL INFORMATION:  
; APPLICANT: Su, Hongsheng  
; APPLICANT: Blain, Francoise  
; APPLICANT: Bennett, Clark  
; APPLICANT: Gu, Kangfu  
; APPLICANT: Zimmermann, Joseph  
; APPLICANT: Musil, Roy  
; TITLE OF INVENTION: Nucleic Acid Sequences And Expression  
; TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From  
; TITLE OF INVENTION: Flavobacterium heparinum  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington, D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC DOS/MS DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/900,951  
; FILING DATE:

CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/258,639  
; FILING DATE: 10 JUNE 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Healey, William J.  
; REGISTRATION NUMBER: 36,160  
; REFERENCE/DOCKET NUMBER: 104385.116  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)942,8400  
; TELEFAX: (202)942,8484

INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 23 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-900-951-9

Query Match 3.5%; Score 124; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 7.9e-05;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 414 VLKASPPGEFFHAQPDNGTGFELFI 436  
Db 1 VLKASPPGEFFHAQPDNGTGFELFI 23

## RESULT 7

PCT-US95-07391A-9  
; Sequence 9, Application PC/TUS9507391A  
; GENERAL INFORMATION:  
; APPLICANT: IBEX TECHNOLOGIES and  
; APPLICANT: ZIMMERMANN, Joseph  
; TITLE OF INVENTION: Nucleic Acid Sequences And Expression  
; TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From  
; TITLE OF INVENTION: Flavobacterium heparinum  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington, D.C.  
; COUNTRY: U.S.A.

ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: IBM PC compatible  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/07391A  
FILING DATE: 09-JUNE-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/258,639  
FILING DATE: 10 JUNE 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BAKER, Hollie L.  
REGISTRATION NUMBER: 31,321  
REFERENCE/DOCKET NUMBER: 104385.116PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)942-8400  
TELEFAX: (202)942-8484  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US95-07391A-9

Query Match 3.5%; Score 124; DB 5; Length 23;  
Best Local Similarity 100.0%; Pred. No. 7.9e-05;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 414 VLKASPPGCFHQAQPDNGTFELPI 436  
DB 1 VLKASPPGCFHQAQPDNGTFELPI 23

RESULT 8  
US-08-258-639A-10  
; Sequence 10, Application US/08258639A  
; Patent No. 5681733  
; GENERAL INFORMATION:  
; APPLICANT: Su, Hongsheng  
; APPLICANT: Blain, Francoise  
; APPLICANT: Bennett, Clark  
; APPLICANT: Gu, Kangfu  
; APPLICANT: Zimmermann, Joseph  
; APPLICANT: Musil, Roy  
; TITLE OF INVENTION: Nucleic Acid Sequences And Expression  
; TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington, D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/258,639A  
FILING DATE: 10 JUNE 1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Healey, William J.  
REGISTRATION NUMBER: 36,160  
REFERENCE/DOCKET NUMBER: 104385.116  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)942-8400

TELEFAX: (202)942-8484  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-258-639A-10

Query Match 3.4%; Score 119; DB 1; Length 23;  
Best Local Similarity 91.3%; Pred. No. 0.00022;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 101 KALVHQFQPHKGYGYFDYDKDIN 123  
DB 1 KALVHFWFPHKGYGYFDYDKDIN 23

RESULT 9  
US-08-900-951-10  
; Sequence 10, Application US/08900951  
; Patent No. 5919693  
; GENERAL INFORMATION:  
; APPLICANT: Su, Hongsheng  
; APPLICANT: Blain, Francoise  
; APPLICANT: Bennett, Clark  
; APPLICANT: Gu, Kangfu  
; APPLICANT: Zimmermann, Joseph  
; APPLICANT: Musil, Roy  
; TITLE OF INVENTION: Nucleic Acid Sequences And Expression  
; TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington, D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/900,951  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/258,639  
FILING DATE: 10 JUNE 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Healey, William J.  
REGISTRATION NUMBER: 36,160  
REFERENCE/DOCKET NUMBER: 104385.116  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)942 8400  
TELEFAX: (202)942 8484  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-900-951-10

Query Match 3.4%; Score 119; DB 2; Length 23;  
Best Local Similarity 91.3%; Pred. No. 0.00022;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 101 KALVHQFQPHKGYGYFDYDKDIN 123  
DB 1 KALVHFWFPHKGYGYFDYDKDIN 23





Db 547 QKYRVRVRYATSVSGLNFVFI----- 567  
QY 476 NONMVITKARONKWT--GNLIDLTY-----TNPSYN-----LDH--QRSVL 515  
Db 568 NDEIALQKNFQSTVETIGEGKD-LTYGSFGYIEYTTTQFPNEHPKITLHLNHLNNSPP 626  
QY 516 FINKKYFLVIDRAIGEATGNLGVHQLKEDSNPVPDKTKNRVYVTVTRDGNLNM--IQSL 572  
Db 627 YVDSIEFIPVD-----VNYDEK-----LEKAQKAVNTLFTGEGNALQKYVTDY 671  
QY 573 NADRTSL 579  
Db 672 KVDQVSI 678  
RESULT 12  
US-07-973-320-4  
; Sequence 4, Application US/07973320  
; Patent No. 5286486  
; GENERAL INFORMATION:  
; APPLICANT: Payne, Jewel M.  
; APPLICANT: Fu, Jenny M.  
; TITLE OF INVENTION: No. 5286486el Bacillus thuringiensis Gene  
; TITLE OF INVENTION: Encoding a Coleopteran-Active Toxin  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/973,320  
; FILING DATE: 19921106  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/788,638  
; FILING DATE: 6-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: MA68.C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1138 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Bacillus thuringiensis  
; STRAIN: kumamotoensis  
; INDIVIDUAL ISOLATE: HD867  
; IMMEDIATE SOURCE:  
; LIBRARY: Lamdagem (TM)-11 library of J.M. Fu  
; CLONE: 867  
US-07-973-320-4

Query Match 3.4%; Score 119; DB 1; Length 1138;  
Best Local Similarity 19.8%; Pred. No. 0.14;  
Matches 132; Conservative 85; Mismatches 206; Indels 244; Gaps 39;

QY 48 NKAVA-----AGNYDDAKALLAYBEKSKAREPDFSNAEKPADIRQIPDKVTREMAKAL 103  
Db 121 NKALAELEGLNN-----LTIYQQ-----ALEDWLNDDPATITRVIDRF--RIILD-AL 167  
QY 104 VHQFQPHKGYGFD-----YCKOINWQM-----WPKVDNEV----- 134  
Db 168 PESYMPFRVAGYEIPLLTVAQAANLHALLRDLSTLYGDKWGFQNNIENYNEQKKHI 227  
QY 135 -RMQLHRVKKWQA-MALVYHATGE-----KYAREWVYQYSDWAR-----KNPLGLSQND 183  
Db 228 SEYSNHCWYNSGLSRLNGSTYEQWYNVNRFRREMILMVLIDIAAVFPIYDPRMYSMTS 287  
QY 184 KEVWR-----PLEVSDRVQSLPPTESLFVNSPAFTAFMEFLNSYHOQADVLSTHYAQ 238  
Db 288 TOLTREVYTDPLSLISNPDIGSPSQMNTAFRPHLV-----DYLDDELYIYT 336  
QY 239 GNHRLF--EAORNLF-----AGVSFPEFKDSRWRGTGIVLNTKIKQVYADGMOFELSP 292  
Db 337 SKYKAFSHEIQPDLFPYCWVKVSPFKKSQSNLY-TTGI-----YGKTSYVSSG 384  
QY 293 IYHVAADIF-----LKAYSKRVNLEKEPPOSYVQTVENMIM 331  
Db 385 AYSFEGNDIYRTLAAPSVVVYPTQNYGVEQVEFYGVKGVHYRGD--NKYDLTYDSIDQ 442  
QY 332 -----ALISISLPDYN-----PMFGDSWITDKNFMQAQFASWARVFP 369  
Db 443 LPPDGEPIHEKYTHRLCHATAISKSTPDYDNATIF--SW-----THRSAEY--YNRYP 494  
QY 370 AN-----QAIKYPATDKQG--KAPNFLSKALSNAGFYTFRSGW--DKNATVMVLKASPP 421  
Db 495 NKIKKIPAKVMKLDLSTVVKGPGFTGGDLVKRG-----SNGYIGDIKATV--NSPLS 546  
QY 422 E-----FHAQPDNGTPELFKGRNFTPDAGVVFVSGDEAIMKLRNWRQTRIHTLTLD 475  
Db 547 QKYRVRVRYATSVSGLNFVFI----- 567  
QY 476 NONMVITKARONKWT--GNLIDLTY-----TNPSYN-----LDH--QRSVL 515  
Db 568 NDEIALQKNFQSTVETIGEGKD-LTYGSFGYIEYTTTQFPNEHPKITLHLNHLNNSPP 626  
QY 516 FINKKYFLVIDRAIGEATGNLGVHQLKEDSNPVPDKTKNRVYVTVTRDGNLNM--IQSL 572  
Db 627 YVDSIEFIPVD-----VNYDEK-----LEKAQKAVNTLFTGEGNALQKYVTDY 671  
QY 573 NADRTSL 579  
Db 672 KVDQVSI 678  
RESULT 13  
US-08-258-639A-2  
; Sequence 2, Application US/08258639A  
; Patent No. 5681733  
; GENERAL INFORMATION:  
; APPLICANT: Su, Hongsheng  
; APPLICANT: Blain, Francoise  
; APPLICANT: Bennett, Clark  
; APPLICANT: Gu, Kangfu  
; APPLICANT: Zimmermann, Joseph  
; APPLICANT: Musil, Roy  
; TITLE OF INVENTION: Nucleic Acid Sequences And Expression  
; TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From  
; TITLE OF INVENTION: Flavobacterium heparinum  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington, D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/258,639A  
FILING DATE: 10 JUNE 1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Healey, William J.  
REGISTRATION NUMBER: 36,160  
REFERENCE/DOCKET NUMBER: 104385.116  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)942-8400  
TELEFAX: (202)942-8484  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 772 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-258-639A-2

Query Match 3.4%; Score 118; DB 1; Length 772;  
Best Local Similarity 20.5%; Pred. No. 0.09;  
Matches 128; Conservative 79; Mismatches 229; Indels 188; Gaps 30;

QY 145 QAMALVYHATGDEKYAREWVYQSD---WARKNPLG-LSQDNDFVWRPLEVSDRV--QS 198  
DB 109 ELMALNYLMTYDKPKVGREAITSIIDTLETATFKAGDISRGIGLFMTGAIYDWCYDQL 168  
QY 199 LPPTFSLFVNS-----PAFTPAFLMEFLNSYHQOAYLSTHYAEQGNHRLFEA 246  
DB 169 KPEKTRFVKAFVRLAKMLECGYPPVKDKSVGHASEMMIMRDLSSVGLAIYDE---PPE 225  
QY 247 QRNLFAGVSPPEFKDSRW-----RQTGISVINTETIKQVYA-----DGM 286  
DB 226 MYNLAAGRFKHEHLVARNWFYPSHNYHQMSYLVNRFNDLFWILDRMGAGNVFNPQG 285  
QY 287 QFELSPIYHVAADIFIKAVGSAKRVNLEKEFPQSYQTVENMIMALISISLPDYNTPMF 346  
DB 286 QFILDYALYKRRPDQILAGD---VDYSRKKPKYYT-----MPALLAGSY--YKDEYL 334  
QY 347 GDSWITDKNFRMAOFASWARVFPANQAIKYFATGKQG-KAPNFLSKAL---SNAGFYTF 402  
DB 335 NYEFLKDPN-----VEPHCKLFEFLWRDTQLGSRKRPDDLPLSRYSGPSFGWMIA 383  
QY 403 RSGWDKNATVMVLKASPPGEF---HAQPDNGTFELFKGRNFTPDAGVFV-YSGDEAIM 457  
DB 384 RTGWPESVIAEMKVN---EYSFLNHQHDAGAFQIYKQ-PLAIDAGSYTGSSGGYNP 439  
QY 458 KLRNRYQTRIHSTLTL-----DNQNMVITKARQ-----486  
DB 440 HKNKFFKRTIAHNSILLIYDPKETSSGYSGSDHTDFAANDGGQELPKGWIAPRDLKEM 499  
QY 487 --NKWETGNL-----DVLTYTPNSYPL-----DHQSRVLPINKK-----520  
DB 500 LAGDFRTGKILAQGFDPNQ---PDYTYLKGDITAAVSAKVSKEKRSFLEFLNLKDAKVP 556  
QY 521 -YELVIDRAGEATGNLGVHQLKEDSNPVDK-----TKNRYVITYTDGNN--566  
DB 557 AAMIVFDKVA-----SNPDPFKFWLHLSIEQPEIKGNQITIKRTKXGDS 601  
QY 567 -----LMIQSLNADRTSLNEEBKVSYYV-----NKLKRPAPVFE-KPKK 606  
DB 602 GMLVNTALLPDAANSNITSIG-GKGKDFWVGTVNDPKFGTDEALERGERWVEITPKK 660  
QY 607 NAGTQNFVSIVPYDG--QKAPBI 628  
DB 661 AAEDYINLVIQIADNTQOKLHEV 684

RESULT 14

US-08-900-951-2

; Sequence 2, Application US/08900951

Patent No. 5919693  
GENERAL INFORMATION:  
APPLICANT: Su, Hongsheng  
APPLICANT: Blain, Francoise  
APPLICANT: Bennett, Clark  
APPLICANT: Gu, Kangfu  
APPLICANT: Zimmermann, Joseph  
APPLICANT: Musil, Roy  
TITLE OF INVENTION: Nucleic Acid Sequences And Expression  
TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From  
TITLE OF INVENTION: Flavobacterium heparinum  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr  
STREET: 1455 Pennsylvania Avenue, N.W.  
CITY: Washington, D.C.  
COUNTRY: U.S.A.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/900,951  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/258,639  
FILING DATE: 10 JUNE 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Healey, William J.  
REGISTRATION NUMBER: 36,160  
REFERENCE/DOCKET NUMBER: 104385.116  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)942 8400  
TELEFAX: (202)942 8484  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 772 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-900-951-2

Query Match 3.4%; Score 118; DB 2; Length 772;  
Best Local Similarity 20.5%; Pred. No. 0.09;  
Matches 128; Conservative 79; Mismatches 229; Indels 188; Gaps 30;

QY 145 QAMALVYHATGDEKYAREWVYQSD---WARKNPLG-LSQDNDFVWRPLEVSDRV--QS 198  
DB 109 ELMALNYLMTYDKPKVGREAITSIIDTLETATFKAGDISRGIGLFMTGAIYDWCYDQL 168  
QY 199 LPPTFSLFVNS-----PAFTPAFLMEFLNSYHQOAYLSTHYAEQGNHRLFEA 246  
DB 169 KPEKTRFVKAFVRLAKMLECGYPPVKDKSVGHASEMMIMRDLSSVGLAIYDE---PPE 225  
QY 247 QRNLFAGVSPPEFKDSRW-----RQTGISVINTETIKQVYA-----DGM 286  
DB 226 MYNLAAGRFKHEHLVARNWFYPSHNYHQMSYLVNRFNDLFWILDRMGAGNVFNPQG 285  
QY 287 QFELSPIYHVAADIFIKAVGSAKRVNLEKEFPQSYQTVENMIMALISISLPDYNTPMF 346  
DB 286 QFILDYALYKRRPDQILAGD---VDYSRKKPKYYT-----MPALLAGSY--YKDEYL 334  
QY 347 GDSWITDKNFRMAOFASWARVFPANQAIKYFATGKQG-KAPNFLSKAL---SNAGFYTF 402  
DB 335 NYEFLKDPN-----VEPHCKLFEFLWRDTQLGSRKRPDDLPLSRYSGPSFGWMIA 383  
QY 403 RSGWDKNATVMVLKASPPGEF---HAQPDNGTFELFKGRNFTPDAGVFV-YSGDEAIM 457  
DB 384 RTGWPESVIAEMKVN---EYSFLNHQHDAGAFQIYKQ-PLAIDAGSYTGSSGGYNP 439

```

458 QY 458 KURNWYRQTRIHSTLTL-----DNQNMVITKARQ----- 488
Db 440 HNKNFKEKTIAHNSLLIYDPKPTSSSGYGGSDHTDFAANDGGQLRPGKWIAPROLKEM 499
QY 487 --NKWETGNNL-----DVLTYTNPSPNL-----DHORSULFINKK----- 520
Db 500 LAGDFERTGKILAQGFDPNQF---PDYTYUKGDITAAYSAKVKEVKRSLFLNLKDQKVP 556
QY 521 -YFLVDRAIGEAATGNLGVHWQLKXDSNPVFDK-----TKNRVVTTYRDGNN-- 566
Db 557 AAMIVFDKVA-----SNPDFKFPWLLHLSIEQPEIKGNQITIKRTKNGDS 601
QY 567 -----LMOSLNDRATSLNEERGKVSYY-----NKEIKRPAFVFE-KPKK 606
Db 602 GMLVNTALLPDAANSNITSIG-GRGKGFVWFGTNTYNDPKFGTDEALERGEMRVEITPKK 660
QY 607 NAGTQNFVSIYVPYDG--OKAPEI 628
Db 661 AAAEDYILNVIQIADNTQOKLHEV 684

RESULT 15
PCT-US95-07391A-2
; Sequence 2, Application PC/TUS9507391A
; GENERAL INFORMATION:
; APPLICANT: IBEX TECHNOLOGIES and
; APPLICANT: ZIMMERMANN, Joseph
; TITLE OF INVENTION: Nucleic Acid Sequences And Expression
; TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived
; TITLE OF INVENTION: Flavobacterium heparinum
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent.in release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07391A
; FILING DATE: 09-JUNE-1995
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/258,639
; FILING DATE: 10 JUNE 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Hollie L.
; REGISTRATION NUMBER: 31,321
; REFERENCE/DOCKET NUMBER: 104385.116PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 942-8400
; TELEFAX: (202) 942-8484
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 772 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-07391A-2

```

169	QY	KPEKTRFVKAFVRLAKMLECGYPPVKDKSVGHASEWMIMRDLLSVGIAIYDE---	FPE	225		
247	QY	QRNLFAGVSPEPKDSRW-----	ROTGISVLNTEIKKQVVA	286		
226	Db	MYNLAAGRFFKEHLVARWVPSYNYHGMGYLYLVRFPTNDIFALWILDMGAGVNPQ	285			
287	QY	QFELSPIYHVAADIFIKAYGSAKRVNLEKEFFPOSYQVOTVENMIMALISISLPDXYNTMF	346			
286	Db	QFILIYDAIKRRPQGIILAGD---	VDYSRKPKKYT-----	MPALLAGSY--YKDEYL	334	
347	QY	GDSWITDKNFERMAQFASWARVFPAQAOLKYFATQKQG--	KAPNFLSKAL---	SNAGFYTF	402	
335	Db	NYEFLKDPN-----	VEPHCKLFEFLWRDTQLGSRKPD	DDLP	LSRYSGSPFGWMTA	383
403	QY	RSWGDKNATVMVLKASPPGEF---	HAQPDNGTGFELFIKGRNFT	PDAGVVF--	YSGDEAIM	457
384	Db	RTWGMPESVIAEMKVN--	EYSFLNHQHODAGAFQIYYKG--	PLAIDAGSYTSGSGGYNSP	439	
458	QY	KLRNYYQTRIHSITLT-----	DQONVUITKARO	-----	486	
440	Db	HNKNFFKRTTAHNSLLIYDPKETS	SSGYGSDHTDFAANDGGQRLPGKGTAPRLDKEM	499		
487	QY	--NKWETGNL-----	DVLTYTNPSPNL-----	DQRSVLFINCK-----	520	
500	Db	LADGFRGTGILLAQCGFDNQI---	PDIYTLKGDITAAYS	AKVKEVRSFLFLNLKDAKYP	556	
521	QY	YFLVIDRAIGTEATGNLGVHQLKEDSNPVDFK-----	TKNRYVITYRDN	601		
557	Db	AAMIVDFDKVA-----	SNPDFKFKFWLLHSIRBQPEIKGNQIT	IKRTKNGDS	601	
567	QY	-----	LMIQSLNADRTSLNEEBGKSVYV-----	NKELKRPAPVEE--	KPKK	606
602	Db	GMLVNTALLPDAANSNITSIG--	GKGKDFWVGTYNTNDPKGTDEALERGEWRV	EITPKK	660	
607	QY	NAGTQNFVSIYPYDGG--	QKRAPEI	628		
661	Db	AAAEYLYNLVIOADNTOOKLHEV	684			

Search completed: July 28, 2003, 20:53:36  
Job time : 31 secs

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XX PR 10-JUN-1994; 94US-0258639.  
XX PA (IBEX-) IBEX TECHNOLOGIES.  
XX PA (ZIMM/) ZIMMERMANN J.  
XX PI Bennett C, Blain F, Gu K, Musil R, Su H, Zimmermann J;  
XX PR WPI; 1996-097381/10.  
XX DR N-PSDB; AAQ99227.  
XX  
XX Nucleic acids encoding Flavobacterium heparinum heparinase II and  
PT III - for degrading heparin and heparan sulphate, also related host  
PT cells, proteins and antibodies, useful in heparinase purificn.  
XX  
XX Claim 16; Fig 9; 75pp; English.  
XX  
XX The sequence corresponds to Flavobacterium heparinum heparinase-III  
CC (EC-4.2.2.8), which degrades heparan sulphate. The sequence is  
CC isolated by polymerase chain reaction amplification using e.g.  
CC primers 3-1 to 3-4 (AAQ99234-099237) or degenerate primers 3-5 to 3-8  
CC (AAQ99238-099241), which are designed based on the sequences of  
CC peptides 3A-3C. Toxicity of the genes and natural selection of  
CC the host against clones with the entire sequence has been  
CC circumvented by cloning sections of the gene separately in  
CC Escherichia coli using a vector with a modified ribosome binding  
CC site, which increases expression levels. The heparinase-III may be  
CC used to neutralise anticoagulant activity. Antibodies against the  
CC protein may be used to differentiate between native and recombinant  
CC enzymes, and when immobilised they may be used for heparinase  
CC purification by affinity chromatography.  
XX  
XX Sequence 659 AA;  
XX  
XX Query Match 100.0%; Score 3494; DB 17; Length 659;  
XX Best Local Similarity 100.0%; Pred. No. 4.8e-279;  
XX Matches 659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 MTTKIFKRIIVFAVIALSSGNILAQSSITRKDPFHINLEYSGLKVNKAVAAGNYDDAA 60  
XX DB 1 MTTKIFKRIIVFAVIALSSGNILAQSSITRKDPFHINLEYSGLKVNKAVAAGNYDDAA 60  
XX  
XX 61 KALLAYREKSKAREPDSNAEKPADIRQIDKVTREMAKALVHQFQPHKGYGFDYDK 120  
XX DB 61 KALLAYREKSKAREPDSNAEKPADIRQIDKVTREMAKALVHQFQPHKGYGFDYDK 120  
XX  
XX 121 DINQWMPVKDNEVRWQLHRVKKWQALVYHATGDEKYAREWYQYSDWARKNPLGLSQ 180  
XX DB 121 DINQWMPVKDNEVRWQLHRVKKWQALVYHATGDEKYAREWYQYSDWARKNPLGLSQ 180  
XX  
XX 181 DNDKFVWRPLEVSDRVQSLPPTFSFLVNSPAFTFAFLMEFLNSVHQQADYLSHYAEOGN 240  
XX DB 181 DNDKFVWRPLEVSDRVQSLPPTFSFLVNSPAFTFAFLMEFLNSVHQQADYLSHYAEOGN 240  
XX  
XX 241 HRLPEAQRNLPAQVSPFEPKDSRWRQTGIVSLNTEIKQYVADQMOPFELSPIHVVAID 300  
XX DB 241 HRLPEAQRNLPAQVSPFEPKDSRWRQTGIVSLNTEIKQYVADQMOPFELSPIHVVAID 300  
XX  
XX 301 IFLKAYGSAKVNLEKEPQSQYVQVTENMIALISLIPDNTFMDGSMITDKNFRMAQ 360  
XX DB 301 IFLKAYGSAKVNLEKEPQSQYVQVTENMIALISLIPDNTFMDGSMITDKNFRMAQ 360  
XX  
XX 361 FASWARVFPANQAIKYFATDGKQKAPNLSKALSNAAGFYTFRSGWKNATVMVLKASPP 420  
XX DB 361 FASWARVFPANQAIKYFATDGKQKAPNLSKALSNAAGFYTFRSGWKNATVMVLKASPP 420  
XX  
XX 421 GEFAQPDNGTFELFIKGRNTTPDAGVFVYSDEAIMKLRNWPYQTRIHSITLTDNQMV 480  
XX DB 421 GEFAQPDNGTFELFIKGRNTTPDAGVFVYSDEAIMKLRNWPYQTRIHSITLTDNQMV 480  
XX  
XX 481 ITKARQNKWETGNLNDVLTNTNPSYPLNDHORSVLFINKYFLVIDRAIGBATGNLGVHW 540  
XX DB 481 ITKARQNKWETGNLNDVLTNTNPSYPLNDHORSVLFINKYFLVIDRAIGBATGNLGVHW 540

QY 541 QLKEDSNPVEDTKNRVYVTVYRDGNNLMIOSLNADRTSLNEEGKVSYYNKLKRPAPV 600  
DB 541 QLKEDSNPVEDTKNRVYVTVYRDGNNLMIOSLNADRTSLNEEGKVSYYNKLKRPAPV 600  
QY 601 FEKPKNAGTQNFVSIYVPYDQKAPETISIRENKGNDFEKGKLNLTITNGKQQLVLVP 659  
DB 601 FEKPKNAGTQNFVSIYVPYDQKAPETISIRENKGNDFEKGKLNLTITNGKQQLVLVP 659  
RESULT 2  
ABP26592  
ID ABP26592 standard; Protein; 634 AA.  
XX AC ABP26592;  
XX DT 02-JUL-2002 (first entry)  
XX DE Streptococcus polypeptide SEQ ID NO 2360.  
XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
XX group A streptococcus; Streptococcus pyogenes; antibacterial;  
XX antiinflammatory; infection; vaccine; meningitis; gene therapy.  
XX OS Streptococcus agalactiae.  
XX PN WO200234771-A2.  
XX PD 02-MAY-2002.  
XX PF 29-OCT-2001; 2001WO-GB04789.  
XX PR 27-OCT-2000; 2000GB-0026333.  
XX PR 24-NOV-2000; 2000GB-0028727.  
XX PR 07-MAR-2001; 2001GB-0005640.  
XX PA (CHIR-) CHIRON SPA.  
XX PA (GENO-) INST GENOMIC RES.  
XX Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;  
XX Tettelin H;  
XX WPI; 2002-352536/38.  
XX DR N-PSDB; ABN67223.  
XX  
XX New Streptococcus protein for the treatment or prevention of infection  
PT or disease caused by Streptococcus bacteria, such as meningitis, and  
PT for detecting a compound that binds to the protein -  
XX  
XX Claim 1; Page 3388; 4525pp; English.  
XX  
XX The invention relates to a protein (ABP25413-ABP30895) from group B  
CC Streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS  
CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in  
CC the specification. The proteins have antibacterial and antiinflammatory  
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and  
CC antibodies that bind (I) are used in the manufacture of medicaments for  
CC the treatment or prevention of infection or disease caused by  
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
CC biological sample. (I) is used to determine whether a compound binds to  
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
CC used as a vaccine or diagnostic composition. The disease caused by  
CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
CC acid encoding (I) may be used to recombinantly produce (I) and may be  
CC used in gene therapy. Antibodies to (I) are used for affinity  
CC chromatography, immunoassays, and distinguishing/identifying  
XX Streptococcus proteins.  
XX  
XX Sequence 634 AA;  
XX  
XX Query Match 7.2%; Score 250.5; DB 23; Length 634;  
XX Best Local Similarity 22.8%; Pred. No. 1e-11;



Db 520 RLISD-CPTTIEETILSKKNYLTSHKLRKFFDKGCTS--TLVAPDPTKVTPTEL 576

Qy 631 RENKGNDFEKGKLNLTLTINGKQ 653

Db 577 OTGKRNPIETA--LSWHLKGKQ 596

RESULT 4  
ABU00675  
ID ABU00675 standard; Protein; 546 AA.  
XX AC  
XX AC ABU00675;  
XX DT 11-FEB-2003 (first entry)  
XX OS S. pneumoniae type 4 strain protein from coding region #242.  
DE  
XX  
XX Bacterial meningitis; pneumonia; sepsis; otitis media;  
KW ear infection; antiinflammatory; antibacterial; immunostimulant;  
KW auditory; respiratory; gene therapy; vaccine.  
XX  
XX Streptococcus pneumoniae type 4 strain.  
OS  
XX WO200277021-A2.  
XX PN  
XX DT 03-OCT-2002.  
XX PD  
XX PF 27-MAR-2002; 2002WO-IB02163.  
XX PR 27-MAR-2001; 2001GB-0007659.  
XX PA (CHIR-) CHIRON SPA.  
XX PA (GENO-) INST GENOMIC RES.  
XX  
XX Masignani V, Tettelin H, Fraser C;  
PI  
XX WPI; 2003-040579/03.  
DR N-PSDB; ABX05954.  
XX  
XX New proteins and nucleic acid molecules from Streptococcus pneumoniae,  
PT useful as medicaments for treating or preventing a disease or infection  
PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media  
PT or ear infection -  
XX  
XX Claim 1; SEQ ID No 484; 56pp; English.  
XX  
XX The invention relates to a protein comprising or having at least 50%  
CC identity to any of the 2469 amino acid sequences, identified in the  
CC specification (available on a computer readable format), or its fragment,  
CC expressed from 2469 of 2489 identified DNA coding regions from the  
CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as  
CC AS956454. Also included are an antibody which binds one of the  
CC proteins, treating a patient by administering the protein, DNA or  
CC antibody (in a composition), a kit comprising first and second primers,  
CC which are the nucleic acid cited above or fragments between nucleotides  
CC 8-100 of a sequence not defined in the specification, for amplifying a  
CC target sequence contained within a Streptococcus nucleic acid sequence,  
CC where the first primer is substantially complementary to the target  
CC sequence and the second primer is substantially complementary to the  
CC complement of the target sequence, and where the parts of the primers  
CC having substantial complementarity define the termini of the target  
CC sequence to be amplified, assay comprising contacting a test compound  
CC with the protein, and determining whether the test compound binds to the  
CC protein and a Streptococcus pneumoniae bacterium, where one or more  
CC genes encoding the proteins has been rendered inactive. The proteins,  
CC nucleic acid molecules, antibody and compositions are useful as  
CC medicaments for treating or preventing a disease or infection due to  
CC streptococcus bacteria, particularly S. pneumoniae, such as pneumonia,  
CC sepsis, otitis media or ear infection. They are also useful in developing  
CC vaccines, diagnostics and antibiotics. The methods are useful for  
CC identifying immunodominant proteins. The present sequence is one of  
CC\* the 2469 proteins expressed by the identified coding regions from the  
CC genomic sequence.

[illegible]

CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX  
SQ Sequence 546 AA;

Query Match 5.0%; Score 176; DB 24; Length 546;  
Best Local Similarity 20.8%; Pred. No. 1.1e-05;  
Matches 117; Conservative 82; Mismatches 231; Indels 132; Gaps 230

QY 71 SKAREPDSNAEKPADIRQPTDKVTRMADKALVHQPHKGYGYDYGDKNINQMWPVK 130  
DB 26 SKDYEKVKSLERLMDNRFPDS-PWDNEPCSKIHQIP-----MWDQVFD 72  
QY 131 DNEVRWQLHRVKKWQAMALVYHATGDEKYAR-----EWYQYSDWARKNPLGUSQND 183  
DB 73 DPEWSYMLNRQYELLQFMIGYLVREGDKDYIQCKFFLPDWTIEQVREFSQSLMTRTLDTG 132  
QY 184 --KEVWEPLVESRVQSILPTTFESLTVNSPAPTPAFLMFEFLNSYHQADYLSHYAEQ--- 238  
DB 133 IRSFTWUKL-----LLLLFLDLEEKELEKILVLSRKQIDFMKSYIRAKYTL 180  
QY 239 GNHRLFAQRNLFAGVPEPKDSPRWKQTGISVLNTEIKQVYADGMQFELSPIYHV-- 296  
DB 181 SNWGILQTIEMLAITYHFESDKMDLEAYHFASEELKQIETQILGDGSGFEQSIYHYEV 240  
QY 297 --RAIDIFLKAYGSAKRVNLEKEFPQSVCQTVENKIMMALISLSLDYNTPEMGDSWITDK 354  
DB 241 YKALLDLCL-----LLPDLQDSYQELLEKNATYIQMWTGLDGRTLAFGSDSTET 290  
QY 355 NFRMAQPA-----SWARVFPANQAIKYFATDGKGQKQAPNPLSKALNA 397  
DB 291 TEILSASVLNQEDLLNGLDVKVDLLSLLFLGREKVKRLQEFEKRAQPK--SMIFEDS 348  
QY 398 GFYTFRGWKNKATVMVLKASPPGEFPAQPNNGTFELIKGNFTPDAGVYVSGDEALM 457  
DB 349 GHVCIKD----EHRFLFFKNGFLGSAHSHSDNSFCLOYQOQPIFIDAGRSY----- 397  
QY 458 KLRNWRQTRI----HSTLTLDNQNMVITKARQ---NKWE-----TGNNLDLVT 499  
DB 398 --REIYERYLLKSAWSHSTCIVDG-----KAPERITGSWEYVEYYPHSLFCHHKREGVH 449  
QY 500 YTNPSY----PNLD--HORSVLFINKKYFLVID--RAIGEATGNLGVHWQLKEDSNPVPD 551  
DB 450 YIEGAYWSARPDLPLYHRKILMLVEDWLLLVDDIRCOGQ-----HEVLTFQF---ILD 499  
QY 552 KTKNRVTTYTRDG--NNLMTQS 571  
DB 500 KD-----VTYQDGGKINQLRWLS 516

RESULT 5  
ABP29975  
ID ABP29975 standard; Protein; 1165 AA.  
XX AC  
XX AC ABP29975;  
XX DT  
XX DT 02-JUL-2002 (first entry)  
XX DE  
XX DE Streptococcus polypeptide SEQ ID NO 9126.  
XX KW  
XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
XX KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
XX KW antiinflammatory; infection; vaccine; meningitis; gene therapy.  
XX OS  
XX OS Streptococcus pyogenes.  
XX EN  
XX EN WO200234771-A2.  
XX FD  
XX FD 02-MAY-2002.  
XX PF  
XX PF 29-OCT-2001; 2001WO-GB04789.



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XX 27-OCT-2000; 2000GB-0026333.
PR 24-NOV-2000; 2000GB-0028727.
PR 07-WAR-2001; 2001GB-0005640.
XX
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX
PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
PI Tettelin H;
XX
DR WPI; 2002-352536/38.
DR N-PSDB; ABN70606.
XX
PT New Streptococcus protein for the treatment or prevention of infection
PT or disease caused by Streptococcus bacteria, such as meningitis, and
PT for detecting a compound that binds to the protein -
XX
PS Claim 1; Page 4034; 4525pp; English.
XX
CC The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (I) may be used to recombinantly produce (I) and may be
CC used in gene therapy. Antibodies to (I) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins.
XX
SQ Sequence 1165 AA;
Query Match 3.9%; Score 137.5; DB 23; Length 1165;
Best Local Similarity 21.2%; Pred. No. 0.051;
Matches 152; Conservative 85; Mismatches 263; Indels 217; Gaps 39;
QY 43 GLEKV-----NKVAAGN---YDDAAKALLAYREKSK-----AREDFPSNAEKPA 85
DB 485 GQEKVWVLDPVAKSLAAWNDATATDDIKTAAAFIDPSKLGPTGLDFAKINFKREDAI 544
QY 86 DIRQPIDKVTREMA-DKALVHQFQPHKG-YGYFDYKDI---NWQMWPVKDNEVRWQLHR 140
DB 545 IYBAHVDFDTSKALEGKLTHTFGTFSFAFVQGLDYKDLGTVHQLLPV-----593
QY 141 VKWQAMALVTHATGDEKYAEWVYQYSDWARKNPLGLSQDNQFVWRPLEVSDRVQSLP 200
DB 594 -----LSYFYANELDKSRSTAYTSSD-----NNYNGVDP---QHYFALS 630
QY 201 PTFSLFVNSBPAFTAFLEFNSVHQQA-----DYLSTHYAEQGNHRIFE-----245
DB 631 GMYSANPNDRALRIELKNLNEIHKRGVGFVDFVYNYHTART---YLFDELPENYHYFM 687
QY 246 -----AQRNLFAGVSFPFKDSRWRQTCISVLNTEIKKQVVADQMQLSPHYVAAID 300
DB 688 NADGTARESFSGGRGLGTTTHMSRRLLVDSITYLIREPK-----VDGFRDMMGDHDAALIE 743
QY 301 IFLKAYGSAKRWLEKEFPQSYQVTVENMIMALISISLPDYNTPMFGDSWIT-----DKNF 356
DB 744 ---QAFKAAKAIN-----PNTIMIGSGWRTYQGDCEKK 773
QY 357 RMAQFASWARVFPANQAIKYFATDKQKQKAPNFLSKALNSAGFYTFRSGWKN---ATVMV 414
DB 774 EIAADQDMWK---ATNTVGVSDDIR-----NTLKSFGFNEGTAAFITGGAKNLEGLFKT 825
QY 415 LKASP-----PG---BFHAQPDNGTF-ELFIKGRNFTPDAGVFVYSGDEALIKLRWY 463
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DB 826 IKAQPGNEADAPGDVVQYIAAHNMLTLHDVIAKSINKDPKV-----AEEEI-----H 873
QY 464 RQTRIHTLTLDNQNMVITKARQNKWETGNLNLVLTNTPSY-----PNLDHQRSV 514
DB 874 KRIRLNTMILTAQCTAFIHSGQ---EYGRTKQLL---NPDKTKASDDKVPN-----KAT 923
QY 515 LF---INKKYFLVIDRAIGEATGNLGVHWQLKES--NPVFDKTKNRVYT-----TYRDN 565
DB 924 LIDAVAQYFYFIHDSYSSDAVNHF--DWAKATDSIAHPISNQTK--AYTQGLIALRRST 979
QY 566 NLMIQSLNAD-----RTSLNEEGKVSY--VYNKELKPAFVFEKPKKNAGTQ 611
DB 980 DAFYKATKAEDVRDVTLLITQAGQDGIQOEDLIMGYQTVASNGDRVAVFV-----NADNK 1033
QY 612 NFVSIV---YFY-----DQKAPEISIRENKGNDFEKGKLNITLTINGKQQLVL 657
DB 1034 TRKVVLPOAYRYLLGAQVLVDAEQAGVTAIAKPKGVQFTKE---GLTIEGLTALVL 1086
XX
RESULT 6
ABP26712
ID ABP26712 standard; Protein; 1174 AA.
XX
AC ABP26712;
XX
DT 02-JUL-2002 (first entry)
XX
DE Streptococcus polypeptide SEQ ID NO 2600.
XX
KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial;
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX
OS Streptococcus pyogenes.
XX
PN WO200234771-A2.
XX
PD 02-MAY-2002.
XX
PF 29-OCT-2001; 2001WO-GB04789.
XX
PR 27-OCT-2000; 2000GB-0026333.
PR 24-NOV-2000; 2000GB-0028727.
PR 07-MAR-2001; 2001GB-0005640.
XX
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX
PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
PI Tettelin H;
XX
DR WPI; 2002-352536/38.
DR N-PSDB; ABN67343.
XX
PT New Streptococcus protein for the treatment or prevention of infection
PT or disease caused by Streptococcus bacteria, such as meningitis, and
PT for detecting a compound that binds to the protein -
XX
PS Claim 1; Page 3410; 4525pp; English.
XX
CC The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
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CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
CC acid encoding (I) may be used to recombinantly produce (I) and may be  
CC used in gene therapy. Antibodies to (I) are used for affinity  
CC chromatography, immunoassays, and distinguishing/identifying  
CC Streptococcus proteins.  
XX  
SQ Sequence 1174 AA;  
  
Query Match 3.9%; Score 137.5; DB 23; Length 1174;  
Best Local Similarity 21.2%; Pred. No. 0.051;  
Matches 152; Conservative 85; Mismatches 263; Indels 217; Gaps 39;  
  
QY 43 GLEKV-----NKAVAGN---YDAAKALIAVYREKSK-----AREPDFGNAEKPA 85  
DB 494 GQEKVWVLDYAKSLAANDATADDIKTAKAFIDSKLGTGLDPAKINNFKREDAL 553  
QY 86 DIRQPIDKVTREMA-DKALVHQFOPHKG-YGYFDYKDI---NQWMPVKDNEVRWOLHR 140  
DB 554 IYEAHRVDFTSKALEGKLTHTPFGTSAFVEQLDYLKDLGVTHVQLLPV-----602  
QY 141 VKWQAMALVYHATGDEKYAREWYQYSDMARKNPLGSDQNDKFVRPLEVSDVQSLP 200  
DB 603 -----LSFYANELDKGRSTAYTSSD-----NNYNGYDP-----OHYFALS 639  
QY 201 PTFSLFVNSPAFTPAFLMEFLNSYHQQA-----DYLSTHYAEQGNHRLF-----245  
DB 640 GMSANFNDPALRIAELKNLVAETHKGMGVIFDVVYNHTART---YLFEDLEPNYYHEM 696  
QY 246 -----AQRNLFAGVFPFEDKSPWRQTSVLNTEIKQYVADGMQFELSPIYHVAID 300  
DB 697 NADGTARESGGRLGTHAMSRRLVDSITLTREPK---VDGFRFDMGDHAAAE 752  
QY 301 IFLKAYGSAKRVNLEKFPQSYQVTENMIMALISILPDYNTPMFGDSMT-----DKNP 356  
DB 753 ---QAFAAKAIN-----PNTIMIGEGWRTYQGDGKK 782  
QY 357 RMAQFASWARVFPANQAIKYFATDGKQKAPNFKLSKALSNAAGYTFRSQWMDKN---ATVMV 414  
DB 783 ELAADQDMK---ATNTVGVSDDIR-----NTLKSFPNEGTAFTGGAKNLEGLFKT 834  
QY 415 LKASP-----PG---EFHAQPNQGTG-ELFIKGRNFTPDAGVVFYSGDEAIMKLNWY 463  
DB 835 IKAQFGNFEADAPGDVVQYIAAHNLTLDHVIASINKDKPV-----ABEEI-----H 882  
QY 464 ROTRIHSTLTDNOMWITKARQNKWETGNMLDVLTYNPSY-----ENLDHORSV 514  
DB 883 KRIRLGNMILTAGTAFIHSGQ---EYGRTKQLL---NPDYKYSDDKVPN---KAT 932  
QY 515 LF---INKKYLVIDRAIGBATGNLGVHWQLKEDS---NPVFDKTKNRVYT---TYRDGN 565  
DB 933 LIDAVAQYVPFIHDSYDSDAVNHF---DWAKATDSIAHPTISNQTK---AYTQGLIALRRST 988  
QY 566 NLMQSLNAD-----RFSLEEGKVSY---VYNKELKRPFAVFEKPKKNAGTQ 611  
DB 989 DAFTKATKAEDVRDVLITQAGQDGIQOEDLIMGYQTVASNGDRIYAVFV-----NADNK 1042  
QY 612 NFVSIV---YPI-----DGKAPESIRENKGNDFEKGKLNLTITNGKQQLV 657  
DB 1043 TRKVVLPQAYELLGAQVILVDAEQAGYTAIAKPKGVQFTKE-----GLTIEGLTALVL 1095  
  
RESULT 7  
ABB06932  
ID ABB06932 standard; Peptide; 25 AA.  
XX  
AC ABB06932;  
XX  
XX 18-JUN-2002 (first entry)  
XX  
XX Flavobacterium heparinum heparinase III peptide SEQ ID NO:3.  
DE  
XX Flavobacterium heparinum; heparinase III; EC 4.2.2.8; HLGAG; tumour;  
KW heparin-like glycosaminoglycan; cancer; metastasis; angiogenesis;  
XX

KW antitumour; cytostatic; antipsoriatic; antiarthritic; vasotropic;  
KW gynaecological; antiinflammatory; anticoagulant; ophthalmological;  
KW antidiabetic; cerebroprotective; arthritis; psoriasis; scleroderma;  
KW diabetic retinopathy; chronic inflammation; prolonged mensuration;  
KW bleeding; neovascularisation; coagulation disorder; cerebral ischaemia;  
KW thromboembolic stroke; enzyme.  
XX  
OS Flavobacterium heparinum.  
XX  
XX WO200166772-A2.  
XX  
XX 13-SEP-2001.  
XX  
XX 08-MAR-2001; 2001WO-US07464.  
XX  
XX 08-MAR-2000; 2000US-187846P.  
XX  
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
XX  
XX Dongfang L, Pojasek K, Shriver Z, Holley K, El-Shabrawi Y;  
XX Venkataraman G, Sasisekharan R;  
XX WPI; 2001-596840/67.  
XX  
XX Novel modified heparinase III polypeptides useful for treating cancer  
XX and inhibiting tumor cell growth and/or metastasis, sequencing  
XX heparin-like glycosaminoglycans, and removing active heparan sulfate  
XX from solution -  
XX  
XX Example 2; Page 52; 94pp; English.  
XX  
XX The present sequence represents a Flavobacterium heparinum heparinase III  
XX (EC 4.2.2.8) peptide, which is used in an example from the present  
XX invention. The present invention describes a substantially pure  
XX heparinase III (H) (modified (H)) (I) having the amino acid sequence of  
XX mature Flavobacterium heparinum (see ABB06931), or having conservative  
XX substitutions within residues non-essential to enzymatic function such  
XX as His residue at positions 36, 105, 110, 139, 152, 225, 234, 241, 424,  
XX 469 or 539 that is substituted by Ala, Ser, Tyr, Thr or Lys residue.  
XX (I) has antitumour, cytostatic, antipsoriatic, antiarthritic, vasotropic,  
XX gynaecological, antiinflammatory, anticoagulant, ophthalmological,  
XX antidiabetic and cerebroprotective activities, and can be used as:  
XX tumour cell proliferation or metastasis inhibitor; a neovascularisation  
XX or angiogenesis inhibitor; and a heparin-like glycosaminoglycans (HLGAG)  
XX cleavage mediator. (I) is useful for preventing proliferation of tumours  
XX such as prostate tumour or melanoma, and for preventing tumour cell  
XX metastasis. (I) is also useful for treating arthritis, psoriasis,  
XX diabetic retinopathy, chronic inflammation, scleroderma, prolonged  
XX mensuration and bleeding by inhibiting neovascularisation or  
XX angiogenesis. It is also useful for treating disorders associated with  
XX coagulation and so can be used in treating cerebral ischaemia and  
XX thromboembolic stroke.  
XX N.B. The sequence data for this patent is not represented in the printed  
XX specification but is based on sequence information supplied by the  
XX European Patent Office.  
XX  
SQ Sequence 25 AA;  
  
Query Match 3.7%; Score 128; DB 22; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.001;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 280 QVYADGMQFELSPIYHVAADIFLK 304  
DB 1 QVYADGMQFELSPIYHVAADIFLK 25  
  
RESULT 8  
ABP38787  
ID ABP38787 standard; Protein; 698 AA.  
XX  
XX AC ABP38787;  
XX

24-JUL-2002 (first entry)  
 Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3632.  
 Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;  
 antibacterial; gene therapy.  
 Staphylococcus epidermidis.  
 US6380370-B1.  
 30-APR-2002.  
 13-AUG-1998; 98US-0134001.  
 14-AUG-1997; 97US-055779P.  
 08-NOV-1997; 97US-064964P.  
 (GENO-) GENOME THERAPEUTICS CORP.  
 Doucette-Stamm LA, Bush D;  
 WPI: 2002-381255/41.  
 N-PSDB; ABN91332.  
 Novel isolated nucleic acid encoding a Staphylococcus epidermidis  
 polypeptide, useful for diagnosing and treating bacterial infections -  
 Disclosure; SEQ ID 3632; 267pp; English.  
 ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading  
 frame (ORF) nucleic acid sequences which encode the amino acid sequences  
 given in ABP35124 to ABP37960. The S. epidermidis sequences have  
 antibacterial activity and can be used in gene therapy. The sequences  
 can also be used in the diagnosis and treatment of bacterial infections,  
 particularly S. epidermidis infections. The sequences can be used to  
 screen for compounds able to interfere with the S. epidermidis life  
 cycle or inhibit S. epidermidis infection.  
 N.B. The sequence data for this patent did not form part of the printed  
 specification, but was obtained in electronic format directly from the  
 USPTO web site.  
 Sequence 698 AA;  
 Query Match 3.6%; Score 126.5; DB 23; Length 698;  
 Best Local Similarity 18.6%; Pred. No. 0.19;  
 Matches 139; Conservative 109; Mismatches 284; Indels 217; Gaps 31;  
 9 IIVFAVIALSSGNI-LAQSSITR--KDPDHINLEYSGLEKVNKAVAGN-----Y 56  
 32 VFIFAIVVRLGLYLQIAQSHYKQLIKNDENIT-----VNESVPRGILDRNGKVLV 83  
 57 DDAKALLAYVREKSKAREPDSNAEKPAD-IRQIDKVTREMAKALVHQFQPHKGYY 115  
 84 DNASMSITYYTRNRTSQKEMLTAKKLDLTKMDTKITER--DK----- 127  
 116 FDYKGDINQWMP-----VKDNEVRWOLHRV--KWWQA 146  
 128 ---KDFWIQWVPFAKLMRKEQLMLEDGTSIQDQFTQLRDKTIGKQLTKKDLQV 183  
 147 MALV-----YHATGEKYAREWVYQSDWARKNPLGLSQND 183  
 184 LAIYREMNAGSLDPQTIKNEDVSEKVAASQQLSKLPGVNTWDRKYPYG---DTL 240  
 184 KFWREPLEVDSQSLPTFSLFVNSPAPFAFLMEFLNSVHQADYLSHYAEQGNHRL 243  
 241 RGIFG--DVSTSTGIPKELT-----EQYLSKGYSRNDRVGKSYLEYQYEDV 285  
 244 FEAQRNLFAGVSFPFKDSPRWQRTGISVLNTEIKKQVYADGMQFELSPIYHVAIDIFL 303  
 286 LKGTQKQM-----KYTTDKSRVLSSEVLNPGSR-----GHDQLT-----IDIDL 326  
 304 KAYGSAKRVN--LEKEFPQSYVQTVENMIMALISLSDYNTPTMFGDSWITDKNFRMAQF 361

Db 327 Q-----KKVBSLLEKQISKLRSQAKMDMDNALMVQPNKNGDILALAGKQIDKQCKLKDY 381  
 QY 362 --ASWARVFPANQAIK-YFATDGKQKAPN-----FLSKALSAGFYFRSGWDKNA--- 410  
 Db 382 DIGNFTAQYTVGSSVKGITLLAGYQKAINVGETWVDEPLKFGQGLTKRSYFNKNGHVS 441  
 QY 411 -----TVMVLKASPPGEPHFAQPDNGTFFELFKGRNFTPDAGVFVYSGDE 454  
 Db 442 DDQALMHSSNVYMFXTALKLAGDPYTGSMLENN-----IADAG----- 481  
 QY 455 AIMKLRNRYQTRIHSITLIDNQNMVITKARQKQWETGNNLDVLTYNPSPYMLDHORSV 514  
 Db 482 --RKLKRLNQVGLKGTGIDLENETPGQIEPTNNPNNYLDLAIGQYDTYTPQLQSQYV 539  
 QY 515 LFINKKYFLV--IDRAIGEATGNLGVHQLKEDSNPVDKTKNRVYTYTYRDGNNLMIQS 571  
 Db 540 STIANDGYRIQPHIGLSIYESTN-----KDETGLKKKIKGNVLNKVNNNSDEIKRV 591  
 QY 572 LNAADRTSLNEEGKVYVYNNKELKRP-----AFVFE--KPKKNAGTQNFVSIVYV--- 619  
 Db 592 QEGFKMAFNEKQG-TGYASFRNTVWPSAGKTGTAEVFGDGEPRVNSTYIGYAPVDPKLS 650  
 QY 620 ----YDGOKAPEISIRENKGNDFEKGKLN 644  
 Db 651 FSIYVYNQVPPPPWL---NGGDLGRDVIN 676

RESULT 9  
 AAR89270  
 ID AAR89270 standard; Peptide; 23 AA.  
 XX  
 AC AAR89270;  
 XX  
 DT 07-APR-1996 (first entry)  
 XX  
 DE Heparinase-III-derived peptide-3B.  
 XX  
 XX Heparinase-III; heparan sulphate degradation; PCR; primer; cloning;  
 KW Escherichia coli; polymerase chain reaction; ribosome binding site;  
 KW toxicity; vector; haemostatic; blood-clotting; antibody;  
 KW affinity chromatography.  
 XX  
 OS Flavobacterium heparinum.  
 XX  
 XX W09534635-A1.  
 PN  
 XX  
 PD 21-DEC-1995.  
 XX  
 PF 09-JUN-1995; 95WO-US07391.  
 XX  
 PR 10-JUN-1994; 94US-0258639.  
 XX  
 XX (IBEX-) IBEX TECHNOLOGIES.  
 PA (ZINW/) ZIMMERMANN J.  
 XX  
 XX Bennett C, Blain F, Gu K, Musil R, Su H, Zimmermann J;  
 PI  
 XX  
 XX WPI; 1996-097381/10.  
 DR  
 XX  
 XX Nucleic acids encoding Flavobacterium heparinum heparinase II and  
 PT III - for degrading heparin and heparan sulphate, also related host  
 PT cells, proteins and antibodies, useful in heparinase purificn.  
 XX  
 XX Example 2; Page 22; 75pp; English.  
 PS  
 CC The sequence corresponds to peptide-3B derived from Flavobacterium  
 CC heparinum heparinase-III (EC-4.2.2.8, AAR89264), which degrades  
 CC heparan sulphate. The sequence, along with peptides 3A (AAR89269)  
 CC and 3C (AAR89271) may be used to construct DNA primers, e.g. 3-1 to  
 CC 3-4 (AAQ99234-Q99237) or degenerate primers 3-5 to 3-8  
 CC (AAQ99238-Q99241), which may be used to isolate the heparinase-III  
 CC gene by polymerase chain reaction amplification. Toxicity

CC of the gene and natural selection of the host against clones with  
 CC the entire sequence has been circumvented by cloning sections of  
 CC the gene separately in *Escherichia coli* using a vector with a  
 CC modified ribosome binding site, which increases expression levels.  
 CC The heparinase-II may be used to neutralise anticoagulant activity.  
 CC Antibodies against the protein may be used to differentiate  
 CC between native and recombinant enzymes, and when immobilised they  
 CC may be used for heparinase purification by affinity chromatography.

XX SQ Sequence 23 AA;

Query Match 3.5%; Score 124; DB 17; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.0019;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 414 VLKASPPGFEHQAQPDNGTFFELFI 436

DB 1 VLKASPPGFEHQAQPDNGTFFELFI 23

RESULT 10

AAV70201

ID AAV70201 standard; Protein; 772 AA.

XX AC AAV70201;

XX DT 06-JUN-2000 (first entry)

XX DE Mutant F. heparinum heparinase II- (6).

XX KW Heparinase II; heparin-like glycosaminoglycan; HLGAG; angiogenesis;  
 KW eye disease; abnormal neovascularisation; psoriasis;  
 KW cellular proliferation; antipsoriatic; cardiant.

XX OS Flavobacterium heparinum.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 347

XX FT /note= "Wild type His substituted by Ala"

XX PN WO200012726-A2.

XX PD 09-MAR-2000.

XX PF 27-AUG-1999; 99WO-US19841.

XX PR 27-AUG-1998; 98US-0098153.

XX PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.

XX PI Shriver Z, Venkataraman G, Sasisekharan R, Liu D;

XX DR WPI; 2000-237884/20.

XX PT Modified heparinases, useful for inhibiting angiogenesis, for  
 PT diminishing the symptoms of psoriasis and for inhibiting cellular  
 PT proliferation, are rationally designed and based on heparinase I and II  
 PT of Flavobacterium heparinum -

XX PS Example 21; Page -, 101pp; English.

XX CC The present sequence is mutant heparinase II with a site-directed  
 CC mutagenesis by overlap extension PCR with 15 cycles. This mutant  
 CC displayed detectable enzymatic activity. Modified heparinases are useful  
 CC for studying structure-function relationship of heparin-like  
 CC glycosaminoglycans and therapeutic purposes. They are also useful for  
 CC removing active heparin from a heparin containing fluid or active  
 CC heparan sulphate from a heparan sulphate containing fluid, where the  
 CC heparinase is immobilised on a solid support. This is used for  
 CC inhibiting angiogenesis in tumour, for treating an eye disease  
 CC characterised by abnormal neovascularisation, psoriasis and for  
 CC inhibiting cellular proliferation. They are also useful for sequencing

CC heparin or heparan sulphate.  
 CC Note: The present sequence is not given in the specification but has  
 CC been derived from heparinase II (AAV70158).

XX SQ Sequence 772 AA;

Query Match 3.5%; Score 124; DB 21; Length 772;

Best Local Similarity 20.7%; Pred. No. 0.36;

Matches 129; Conservative 79; Mismatches 228; Indels 188; Gaps 30;

QY 145 QAMALVYHATGDEKYAREWVYQYSD---WARKNPLG-LSQNDKFXVRPLEVSDRV--QS 198

DB 109 ELMALNYLMTKDPKVGREAITSIIDTLETATATFKAGDISRGIGLFWMTGAIYDWCYDQL 168

QY 199 LPPTFSLFVNS-----PAFTPAFLMEFLNSVHQQADYLSHYAQQGNHRLFEA 246

DB 169 KPBEKTRFVKAFLVRLAKMLECGYPPVKDKSIIVGHASEWIMNRDLSVGIAYDE---FPE 225

QY 247 QRNLFAGVSFPEFKDSPW-----RQTGISVLNTEIKKQVYA-----DGM 286

DB 226 MYNLAAGRFFKEHLVARNWVFPYSHNYHQGMSYLVNVRTNDLFAWLDRMGAGNVFPCQ 285

QY 287 QFELSPIYHVAIDIFLKAYGSAKRVNLEKEFPQSYQTVENMALLISILPDYNTPMF 346

DB 286 QFILIYDAIYKRRPDGQILAGGD---VDYSRKKPKYIT---MFALLAGSY--YKDEYL 334

QY 347 GDSMTTDKNFRMAQFASWARVFPANQAIKYFATDGKQG-KAPNFLSKAL---SNAGFYTF 402

DB 335 NYEFLKDPN-----VEPACKLFEFLWRDTQLGSRKPDPLPLSRYSGPSFGWMTA 383

QY 403 RSGMDKNATVMVLKASPPGEF---HAQPDNGTFFELFKGRNFTPDAGVTV--YSGDEALM 457

DB 384 RTGWPESVIAEMKVN---EYSFLNHQHDAGAFQIYKKG-PLAIDAGSYTSGSGYNSP 439

QY 458 KLRNRYQRTIHSITLTL-----DNQNMVITKARQ-----486

DB 440 HKNKFFKRTIAHNSLLIYDPKETFSSGYGSDHTDFAANDGGQRLPGKGTAPRDLKEM 499

QY 487 --NKWETGNL-----DVLTYTNESYPNL-----DHQRSYLVFINKK-----520

DB 500 LAGDRTGKILAQGFGPDNQT---PDYTYLKGDITAAVSAKYKVKRSFLFLNLKDAKVP 556

QY 521 -YFLVIDRAIGEATGNLGVHWQLEDSNPVFDK-----TKNRYVITYRQNN--566

DB 557 AAMIVFDKVA-----SNPDFKKFWLLHSIEQPEIKGNQITIKRTKNGDS 601

QY 567 -----LMIQSLNADRTSLNEEGKVSYVY-----NKLKPEAFVE-KPKK 606

DB 602 GMLVNTALLPDAANSNITSIG-GKGKDFWVFGTNTYNDPKGTDEALERGEWRVEITPKK 660

QY 607 NAGTQNFVSIVVPYDG--QKAPEI 628

DB 661 AAADYILNVIQIADNTQOKLHEV 684

RESULT 11

AAV40020

ID AAV40020 standard; Protein; 532 AA.

XX AC AAV40020;

XX DT 30-NOV-1991 (first entry)

XX DE Saccharomyces cerevisiae invertase.

XX KW Signal sequence; invertase; vector; leukocyte interferon.

XX OS Saccharomyces cerevisiae.

XX PN EP127304-A.

XX PD 05-DEC-1984.



[illegible]

DEPT. T 13

RESULT IS  
AAV70170

AAV70170  
ID AAV70170 standard; Protein: 772 AA.

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DT	06-JUN-2000	(first entry)
XX		
DE		Modified F. heparinum heparinase II (1).
DE		
XX		
KW		Heparinase II; heparin-like glycosaminoglycan; HLGAG; angiogenesis;
KW		eye disease; abnormal neovascularisation; psoriasis;
KW		cellular proliferation; antipsoriatic; cardiant.

**XX**

OS Flavobacter:

OS Synthetic.

XX  
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FH	Key	Location/Qualifiers
FH		

Misc-difference

FT	PINC ATTORNEY	/lab
ET		

XX  
T1  
/ TADGET= F118,

XX PN WO2000012726-A2.

FN  
XX  
MOZ00012/Z09-AZ.

09-MAR-2000  
XX PDFD  
YY  
09-MAR-2000.

27-AUG-1999; 99WO-US19841.  
27-AUG-1998; 98US-0098153.  
(MASI ) MASSACHUSETTS INST TECHNOLOGY.  
Shriver Z, Venkataraman G, Sasisekharan R, Liu D;  
WPI: 2000-237884/20.

Cys348 causes heparinase II to become exclusively a heparan sulphate degrading enzyme. Modified heparinases are useful for studying structure-function relationship of heparin-like glycosaminoglycans and therapeutic purposes. They are also useful for removing active heparin from a heparin containing fluid or active heparan sulphate from a heparan sulphate containing fluid, where the heparinase is immobilised on a solid support. This is used for inhibiting angiogenesis in tumour, for treating an eye disease characterised by abnormal neovascularisation, pteriasis and for inhibiting cellular proliferation. They are also useful for sequencing heparin or heparan sulphate. Note: The present sequence is not given in the specification but has been derived from heparinase II (AAV70158).

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Seq	Sequence	772 AA;	Query Match	3.4%;	Score 120;	DB 21;	Length 772;
	Best Local Similarity	20.5%;	Pred. No. 0.76;				
	Matches 128;	Conservative	79;	Mismatches 229;	Indels 189;	Gaps 30	

Qy	145	QAMALVTHATCDEKAYEBWVYQYSD---	WAEKNPLG-LSQDNDFVWRPLEYSDRV--	QS	198
Db	109	ELMALNLTMTKDPKVGREATISIIDTETATFKAGDISRGIGLPMVTGAIYDWCYDOL			168
Qy	199	LPPTFSLFVNS-----	PAFTPAFLMEFLNSYHQADYLSTHYAEOGNHRLFEA		246
Db	169	KPEKTRFVKAFVRLAKMLECGYPPVKDKSIVGHASEWMNRDLLSVGIAIYDE---	PPE		225
Qy	247	QRNLFAGVSPPEFKDPSRW-----	ROTGISVLATEIKKQVYA-----	DCM	286
Db	226	MYNLAAGRFFKEHLIVARNWFVPSNHYHQGMSYLVNFTNDLFAULWILDMRGAGNVFNPGQ			285
Qy	287	QFELSPIYHVAADIFLKAYGSAKRVLNKEKFFPOSYQVTENVIMINALISISLDPYNTPMF			346
Db	286	QFILIYDAIKRRPDQJILAGSD--	VDYSRKPKYYT-----	MPALLAGSY--	YKDEYL 334
Qy	347	GDSWITDKNFRMAQFASWARVFPANQAIKYFATDGKQG--	KAPNFLSKAL--	SNAGFYTF	402
Db	335	NYEFLKDPN-----	VEPHXKUFEFUWRDTQLGSRKPDIDLPSRYSGSPFGWMIA		383
Qy	403	RSQWDKNATVMVLKASPPGEF---	HAQPDNGTFFELFIKGRNFTPDAGVVF--	YSGDEAIM	457
Db	384	RTGWGPESVIAEMKVN--	EYSFLNHQHDAGAFQIYYKG--	PLAIDAGSYTSGSGGYNSP	439
Qy	458	KLRNWWYQTRIHSYTLT---	DNQNMVITKARQ-----		486
Db	440	HNKNFFKRTIAHNSLLIYDPKETSSGYGSDHTDFAANDGGQBLPGKGTAPDLKEM			499
Qy	487	--NKWETGNL---	DVLTYTPSYENL-----	DHORSVLFINKK---	520
Db	500	LADFRGTGKILAQCGFPDQOT---	PDYTYLKGDITAAYSAKYKEVKESFLNLKDAKVP		556
Qy	521	YFLVIDRAIGEATGNLVGHQWKEDSNVPFDK---		TKNRYVITYRDGNN---	566
Db	557	AAMIVFDKVA-----	SNPDFKFKFWLLHSIEQPEIKGNQITTKRTKNGDS		601
Qy	567	-----	LMIOSLNADRTSLNEEGKSVYV-----	NKELKRPAPVFE--	KPKK 606
Db	602	GMLVNTALLPDAANSNITSIG--	GKQKDFWVGTVNTNDFPKCTDDBALERGEWEVETPKK		660
Qy	607	NAGTQNFVSIVPYDYG--	QKAPEI		628
Db	661	AAAEYDLNVQIADNTQOKLHEV			684

RESULT 14

RESOLUTION  
AAR89271

AA89271  
IN AA89271 standard: peptide: 23 AA.

AA89271

XX  
C  
X

AC  
v v  
AAR89271;

XX Heparinase-III; heparan sulphate degradation; PCR; primer; cloning;  
 KW Escherichia coli; polymerase chain reaction; ribosome binding site;  
 KW toxicity; vector; haemostatic; blood-clotting; antibody;  
 KW affinity chromatography.  
 XX Flavobacterium heparinum.  
 XX WO9534635-A1.  
 XX 21-DEC-1995.  
 XX 09-JUN-1995; 95WO-US07391.  
 XX 10-JUN-1994; 94US-0258639.  
 XX (IBEX-) IBEX TECHNOLOGIES.  
 XX (ZIMM/) ZIMMERMANN J.  
 XX Bennett C, Blain F, Gu K, Musil R, Su H, Zimmermann J;  
 XX WPI; 1996-097381/10.  
 XX Nucleic acids encoding Flavobacterium heparinum heparinase II and  
 PT III - for degrading heparin and heparan sulphate, also related host  
 PT cells, proteins and antibodies, useful in heparinase purificn.  
 XX Example 2; Page 22; 75pp; English.  
 XX The sequence corresponds to peptide-3A derived from Flavobacterium  
 CC heparinum heparinase-III (EC-4.2.2.8, AAR89264), which degrades  
 CC heparan sulphate. The sequence, along with peptides 3A (AAR89269)  
 CC and 3B (AAR89270) may be used to construct DNA primers, e.g. 3-1 to  
 CC 3-4 (AAQ9234-Q99237) or degenerate primers 3-5 to 3-8,  
 CC (AAQ9238-Q99241), which may be used to isolate the heparinase-III  
 CC gene by polymerase chain reaction amplification. Toxicity  
 CC of the gene and natural selection of the host against clones with  
 CC the entire sequence has been circumvented by cloning sections of  
 CC the gene separately in Escherichia coli using a vector with a  
 CC modified ribosome binding site, which increases expression levels.  
 CC The heparinase-II may be used to neutralise anticoagulant activity.  
 CC Antibodies against the protein may be used to differentiate  
 CC between native and recombinant enzymes, and when immobilised they  
 CC may be used for heparinase purification by affinity chromatography.  
 XX SQ Sequence 23 AA;  
 Query Match 3.4%; Score 119; DB 17; Length 23;  
 Best Local Similarity 91.3%; Pred. No. 0.005;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 101 KALVHQFQPHKGYGFDYGDKN 123  
 Db 1 KALVHWFHPHKGFDYGDKN 23  
 RESULT 15  
 AAY70171  
 ID AAY70171 standard; Protein; 772 AA.  
 XX AAY70171;  
 XX 06-JUN-2000 (first entry)  
 XX Modified F. heparinum heparinase II (2).  
 XX Heparinase II; heparin-like glycosaminoglycan; HLGAG; angiogenesis;  
 KW eye disease; abnormal neovascularisation; psoriasis;  
 KW cellular proliferation; antipsoriatic; cardiant.  
 XX Flavobacterium heparinum.  
 OS Synthetic.  
 XX

FH Key Location/Qualifiers  
 FT Misc-difference 348  
 XX /note= "Wild type Cys substituted by Ala"  
 PN WO200012726-A2.  
 XX 09-MAR-2000.  
 XX 27-AUG-1999; 99WO-US19841.  
 XX 27-AUG-1998; 98US-0098153.  
 XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
 XX Shriver Z, Venkataraman G, Sasisekharan R, Liu D;  
 DR WPI; 2000-237884/20.  
 XX Modified heparinases, useful for inhibiting angiogenesis, for  
 PT diminishing the symptoms of psoriasis and for inhibiting cellular  
 PT proliferation, are rationally designed and based on heparinase I and II  
 PT of Flavobacterium heparinum -  
 XX Claim 15; Page -; 101pp; English.  
 XX The present sequence is a modified heparinase II isolated from the  
 CC periplasm of Flavobacterium heparinum. Conservative substitutions at  
 CC Cys348 causes heparinase II to become exclusively a heparan sulphate  
 CC degrading enzyme. Modified heparinases are useful for studying structure  
 CC -function relationship of heparin-like glycosaminoglycans and  
 CC therapeutic purposes. They are also useful for removing active heparin  
 CC from a heparin containing fluid or active heparan sulphate from a  
 CC heparan sulphate containing fluid, where the heparinase is immobilised  
 CC on a solid support. This is used for inhibiting angiogenesis in tumour,  
 CC for treating an eye disease characterised by abnormal  
 CC neovascularisation, psoriasis and for inhibiting cellular proliferation.  
 CC They are also useful for sequencing heparin or heparan sulphate.  
 CC Note: The present sequence is not given in the specification but has  
 CC been derived from heparinase II (AAY70158).  
 XX SQ Sequence 772 AA;  
 Query Match 3.4%; Score 119; DB 21; Length 772;  
 Best Local Similarity 20.5%; Pred. No. 0.92;  
 Matches 128; Conservative 79; Mismatches 229; Indels 188; Gaps 30;  
 QY 145 QMALVYHATGDEKYAREWVQYSD---WARKNPLG-LSQDNDKFWRLVSDRV--QS 198  
 Db 109 ELMALNYLMTKDPKVGREAITSIIDTLETATPKPGDISRGIGLPMVTGAIVDYDQ 168  
 QY 199 LPPTFSLFVNS-----PAFTPAFLMEFLNSYHQADYLSLTHVAEQGNHLEFA 246  
 Db 169 KPEETRFVKAFVRLAKMLECGYPPVKOKSIVGHASEWIMEDLLSVGAIYDE---PFE 225  
 QY 247 QRLNLAGVSPFEKDSRW-----ROTGISVLNTEIKKQVYA-----DGM 286  
 Db 226 MYNLAAGRFKEHLVARNWVPSHNYHQGMSYLVNRETNDFALWILDRMGAGNVFNQ 285  
 QY 287 QFELSPIYHVAIDIFLKAYGSAKVNLEKFPQSVQTVENMIMALISLIDVNTPMF 346  
 Db 286 QFILDYAIKRRPDQIILAGD---VDYSRKKPKYTT-----MPALLAGSY--YKDEYL 334  
 QY 347 GDSMTIDKNFRMAQFASWARVFPANQALKYFATGKQG-KAPNFLSKAL---SNAGFYTF 402  
 Db 335 NVEFLKDPN-----VEPHAKLEFELWRDTQLGSRKPDPLLSRYSGSPGWMIA 383  
 QY 403 RSGHDKNATVMVLKASPPGEF---HAQPDNGTFELFIKGRNFTPDAGVFV-YSGDEAIM 457  
 Db 384 RTGWPESVIAEMKVN---EYSFLNHQHDQAGAFQIYKG-PLAIDAGSYTCSSGGYN 439  
 QY 458 KLRNMYRQTRHSTLT-----DNQNMVITKARQ----- 486  
 Db 440 HKNKFFKRTIAHNSLLIYDPKETFSSSGYGGSDHTDFAANDGGQRLPKGWIAPDLKEM 499

